

1	74.4	12.5	372	7	US-10-282-122A-25335	Sequence 25335, A	
2	50	8.4	2466	6	US-10-156-761-5788	Sequence 5788, Ap	
3	50	8.4	9025608	6	US-10-156-761-1	Sequence 1, Appli	
C	4	8.0	2256646	7	US-10-470-565-1	Sequence 1, Appli	
5	47.6	7.9	548	7	US-10-437-963-94550	Sequence 94550, A	
6	46.6	7.8	1389	8	US-10-411-910A-255	Sequence 255, App	
7	46.6	7.8	1389	8	US-10-411-910A-257	Sequence 257, App	
8	46.2	7.7	1209	6	US-10-369-493-32038	Sequence 32038, A	
9	46.2	7.7	1509	8	US-10-411-910A-264	Sequence 264, App	
C	10	45.8	7.7	2238	7	US-10-437-963-69229	Sequence 69229, A
11	45.2	7.6	2238	7	US-10-437-963-97363	Sequence 97363, A	
12	45.2	7.6	3743	9	US-10-502-351-1	Sequence 1, Appli	
13	44.4	7.4	1445	7	US-10-437-963-35783	Sequence 35783, A	
C	14	44.2	7.4	1000	7	US-10-389-566-49	Sequence 49, Appl
15	44.2	7.4	1377	6	US-10-369-493-39791	Sequence 39791, A	
16	44.2	7.4	1395	6	US-10-369-493-39403	Sequence 39403, A	
17	44.2	7.4	1404	6	US-10-369-493-39036	Sequence 39036, A	
18	44.2	7.4	2055	7	US-10-389-566-235	Sequence 235, App	
19	44	7.4	1368	7	US-10-437-963-7459	Sequence 7459, Ap	
20	44	7.4	9338	10	US-11-097-143-32926	Sequence 32926, A	
21	43.8	7.3	1507	8	US-10-425-115-108376	Sequence 108376, A	
22	43.8	7.3	2978	8	US-10-739-930-4715	Sequence 4715, Ap	
23	43	7.2	681	7	US-10-767-701-23705	Sequence 23705, A	

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; TYPE: DNA
; ORGANISM: Legionella pneumophila
US-10-282-122A-25335

Query Match
Best Local Similarity 12.5%; Score 74.4; DB 7; Length 372;
Matches 175; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 68 TGTTTGTATGACCTGGCGGCGCAGAGGATGAGCTGGCGGTTTGACACCTTCTTACGATA 127
Db 14 TGTTTGTATGACCTGGCGGCGCAGAGGATGAGCTGGCGGTTTGACACCTTCTTACGATA 73
Qy 128 AGTGCTGGCTGACCCGCGAGCTGTGCTCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGA 187
Db 74 AAATGCTCATGATGACAGAGTGAATTTATTTTGTATGACGCTGATGAGCAACA 133
Qy 188 AGATGAAGCAGGTCAAGTTCATGAGCTTCGTTTGGCGGAGCAGACCAATACAGGGCC 247
Db 134 TCCTTAAGCAAAAAGGATTTTAAACCATGGTGTGTTGGCGGACCAAAATCAATACACTGAA 193
Qy 248 GAGCATGTACGCGCACCGCCCATCTGTCAGGCGCCACGCGCTGGACACCGCCACT 307
Db 194 AAAGTATGCGGAAGGACATCAGCATCTACT--TGCACAGAGGCTTAAATGACTTCATG 250
Qy 308 TTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATG 367
Db 251 TGGATATGTAATCGAGCATTTAGGGGAACCTTAAGGAATTTGGCGCCCAATGAAGAGG 310
Qy 368 TGATCCAGCAGCGCGCGGAGTGG 391
Db 311 ACATTCAGAAAGTAGTGCATCG 334

RESULT 2
US-10-156-761-5788
; Sequence 5788, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5788
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2466)
US-10-156-761-5788

Query Match
Best Local Similarity 8.4%; Score 50; DB 6; Length 2466;
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

Qy 115 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Db 421 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Qy 175 ATGAAGAGCAGAGATGAAGCAGGTCAAGTTCAATGAGCTTCGTTTGGCGGAGCAGAC 234
Db 175 ATGAAGAGCAGAGATGAAGCAGGTCAAGTTCAATGAGCTTCGTTTGGCGGAGCAGAC 234

Query Match
Best Local Similarity 8.4%; Score 50; DB 6; Length 9025608;
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

Qy 115 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Db 7015347 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Qy 175 ATGAAGAGCAGAGATGAAGCAGGTCAAGTTCAATGAGCTTCGTTTGGCGGAGCAGAC 234
Db 7015407 CTGCTGACGACGAGTTTCTCCACCGGCAACACGCTTCTTCACACCATCCGCGACCTGCAC 7015466
Qy 235 CAATACAGGGCGGAGCAGATGATGAGCAGCAGCCCATCTGTCAGGGCCGCGGCTG 294
Db 7015467 GAGCGCTATCCGCGCGCGGATGATGAGCAGCAGCCCATCTGTCAGGGCCGCGGCTG 294
Qy 295 GACCAACCGCCACTTTGACAAAGATCAAGCAGTACTTGGAGAGAGCGCTGCAAGAGATGGGC 354
Db 7015527 GACCTCGGGCGCTTGGAGCAGTTTCGCGCGGAGATCGTTCGCGGGTGGACCTGATCAGC 7015586
Qy 355 GTCAAGCAGATGTGATTCACAGCAGCGCGCGGAGTGTGAGTCCACCCCGGAGCAATTT 414
Db 7015587 GCGCGCTCGGGGACGCTGAAGCTGCCCGAGGGCGTGTGAGAGAGGGGCGAGAGCTGGTC 7015646
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Db 481 CTGCTCGACGACGAGTTCTCCACCGCAACACGCTTCTCAACACCATCCGCGACCTGCAC 540
Qy 235 CAATACAGGGCGGAGCAGATGATGAGCAGCAGCAGCCCATCTGTCAGGGCCGCGGCTG 294
Db 541 GAGCGCTATCCGCGCGCGGATGATGAGTTCGCTCGCCCTCGTGACATGCTCCCGGCGC 600
Qy 295 GACCAACCGCCACTTTGACAAAGATCAAGCAGTACTTGGAGAGAGCGCTGCAAGAGATGGGC 354
Db 601 GACCTCGGGCGCTTGGAGCAGTTTCGCGCGGAGATCGTTCGCGGGTGGACCTGATCAGC 660
Qy 355 GTCAAGCAGATGTGATTCACAGCAGCGCGCGGAGTGTGAGTCCACCCCGGAGCAATTT 414
Db 661 GCGCGCTCGGGGACGCTGAAGCTGCCCGAGGGCGTGTGAGAGAGGGGCGAGAGCTGGTC 720
Qy 415 GACTTNCCCAACAACCTGCGCAC 437
Db 721 GCCCGCAACAGAGGGCGGTACC 743

RESULT 3
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match
Best Local Similarity 8.4%; Score 50; DB 6; Length 9025608;
Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

Qy 115 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Db 7015347 ACCTTCTACGATAGGTGCTGGCTGACCCGCGAGCTGTCCTTCTTCGAGTCCCTGGAC 174
Qy 175 ATGAAGAGCAGAGATGAAGCAGGTCAAGTTCAATGAGCTTCGTTTGGCGGAGCAGAC 234
Db 7015407 CTGCTGACGACGAGTTTCTCCACCGGCAACACGCTTCTTCACACCATCCGCGACCTGCAC 7015466
Qy 235 CAATACAGGGCGGAGCAGATGATGAGCAGCAGCCCATCTGTCAGGGCCGCGGCTG 294
Db 7015467 GAGCGCTATCCGCGCGCGGATGATGAGCAGCAGCCCATCTGTCAGGGCCGCGGCTG 294
Qy 295 GACCAACCGCCACTTTGACAAAGATCAAGCAGTACTTGGAGAGAGCGCTGCAAGAGATGGGC 354
Db 7015527 GACCTCGGGCGCTTGGAGCAGTTTCGCGCGGAGATCGTTCGCGGGTGGACCTGATCAGC 7015586
Qy 355 GTCAAGCAGATGTGATTCACAGCAGCGCGCGGAGTGTGAGTCCACCCCGGAGCAATTT 414
Db 7015587 GCGCGCTCGGGGACGCTGAAGCTGCCCGAGGGCGTGTGAGAGAGGGGCGAGAGCTGGTC 7015646
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QY 415 GACTTNCCCAACAAGTGGCCACC 437  
Db 7015647 GCCCGCACGAGAGGGCCGTACC 7015669

RESULT 4  
US-10-470-565-1/c  
; Sequence 1, Application US/10470565  
; Publication No. US20040126870A1  
; GENERAL INFORMATION:  
; APPLICANT: Societe des Produits Nestle S.A.  
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium  
; FILE REFERENCE: 80290/NO  
; CURRENT APPLICATION NUMBER: US/10/470,565  
; PRIOR FILING DATE: 2003-07-29  
; PRIOR APPLICATION NUMBER: EP 01102050.0  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2256646  
; TYPE: DNA  
; ORGANISM: Bifidobacterium longum  
US-10-470-565-1

Query Match 8.0%; Score 47.6; DB 7; Length 2256646;  
Best Local Similarity 44.6%; Pred. No. 0.003;  
Matches 185; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

QY 15 CCGCGCCACCAGCAGCAGACGGCGGAGGGGATGGGGCGGCAAGAGCTGTTGA 74  
Db 1432814 CGTCTCTACTTTCACCGCAGGATGGGCTATGAGTGGCCACAGGCAACCCCAAGAACGT 1432755

QY 75 TGACCTGGCGGCGCAGAGGATGAAGCTGGGTTGACACTTCTAGTAAGTGCT 134  
Db 1432754 CGATGAAGAACGACTGTGGGGTCTGAACGTTCCGCTCGAGACCGGACCGCTCGAGGAAGA 1432695

QY 135 GGCTGACCCGGAGCTGTGCTCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAA 194  
Db 1432694 GGCCATCAACAGACCGCCAGCAGTGCAGGCGGACGCGCAGAGACATCACCATCCA 1432635

QY 195 GAAGTGAAGTTCATGAGTTCGTGTTGGCGAGCAGACCAATACAGGGCCGAGAGAT 254  
Db 1432634 GTCTCTCAAGCAGCAGACCGACGCCACCACTGTGTGGTACCGGCAAGCGCGAGCTTT 1432575

QY 255 GTACGACGACACGCCCATCTGTTCAGGGCCAGCGCTGGACCCAGCCGCTTTGACAA 314  
Db 1432574 CTTCCGCGATTCCTCCGGTTGTGCGGTACGCCCATCGCCAGACCGATGGTCACTGGAACA 1432515

QY 315 GATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGAGTGTGATCCA 374  
Db 1432514 GCTCGGCAAGGACTTCGATGAAGTGCAGACGCCATCGCCATCAGAGAGGGCGATTCCTCA 1432455

QY 375 GCACGCGCGCGAGTGGTGGATTCACCGCGCAGCAATTTGACTTNCCCAAC 429  
Db 1432454 GACCACCGAAGCGCTGCAGAGGCCATCAAAAGCTCATGGACGCGGCACCTAC 1432400

RESULT 5  
US-10-437-963-94550  
; Sequence 94550, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazov, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 94550  
; LENGTH: 548  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_9282C.1  
US-10-437-963-94550

Query Match 7.9%; Score 47.4; DB 7; Length 548;  
Best Local Similarity 50.4%; Pred. No. 0.0027;  
Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 216 CGTGTTCGCGGAGCAGACCAATACAAGGCGCGAAGCATGTACGACGACGACGCGCCATCT 275  
Db 194 CGTGTTCGCGGCGCCGACGCGCGCTCGGGCGGGCATGTTCCGCGACCTCGCCCGCTG 253

QY 276 GGTCAAGGGCCACGCGCTGGACACCGCCACTTTTGACAAGATCAAGCAGTACTTTGGAGA 335  
Db 254 GTCATGCTCCACATGCTCAACTTCACGAGGCGGTGACCATGACGAAGCGCGCGCA 313

QY 336 GACGCTGCAAGAGATGGCGCTCAAGCAGAGTGTGATCAGACGCGCGCGGAGTGGTGA 395  
Db 314 GAAGCTCTTCAAGTGTCTGACATGTACGAGGCCACCGCGCGAGTCTCCCGTCTATCGA 373

QY 396 GTCCACCGCGCAGCAATTTGACTTNCCTCAACAACTGCGCACCCAC 441  
Db 374 CGCTTCTCCACCGCGCAGCAGCGCAACACAGCAGCACCCTGACC 419

RESULT 6  
US-10-411-910A-255  
; Sequence 255, Application US/10411910A  
; Publication No. US2004020256A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillon, Harrison F.  
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes  
; FILE REFERENCE: H2041203-P  
; CURRENT APPLICATION NUMBER: US/10/411,910A  
; CURRENT FILING DATE: 2003-04-12  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 255  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-411-910A-255

Query Match 7.8%; Score 46.6; DB 8; Length 1389;  
Best Local Similarity 44.9%; Pred. No. 0.0065;  
Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;

QY 40 GCGAAGCGGATCGGGCGCAAGAAAGCTGTTGATGACCTGGGGCGGCGCAGAAAGCATG 99  
Db 685 GTGGTGGTGGCCCTGCTACGACAGAGCTGGAGGCCCTGCGGAGGGCTGAGCACC 744

QY 100 AAGCTGGCGTTGACACTTTTACGATAAGTGTGTGGTGCACCGGAGCTGTGCCCTTC 159  
Db 745 ACCCTGAACGGCGCGCGGCAACCGACTGCTGTGACGAGCGGCGAGATGCCCGAGATC 804

QY 160 TTCAGTCCCTGGACATCAAGACGAGAGATGAAGAGGTCAAGTTCATGAGCTTCGTG 219  
Db 805 ATGGAGCAGAGCGACCTGAGCGTGAAGGACATCGCCGTGGAGACACCTGTTCGGGACATG 864

QY 220 TTTCGCGAGCAGACCAATACAAGGGCGCAAGAGTGTACGACGACGACGCCCATCTGGTC 279  
Db 865 AAGGAGTGGCGTGCACGGCCACGACGCGGTGACGAGCAGCGCCACTGTGCCCACTGTC 924

QY 280 AAGGGCCACGCGCTGGACCAACCGCCACTTTTGACAAGATCAAGCAGTACTTTGGAGAGCG 339

Db 925 TTCCGCCACGCCCAAGGAGCTGTTTCGGGAGCAGCTGGAGGAGATCACTACCGCGC 984  
QY 340 CTGCAAGAGATGGCGCTCAGCAGGATGTATCAGACGCCCGCGAGTGGTGGATCC 399  
Db 985 CTGCGCAACAGGACTTCCACGAGGTGACCTCGAAGAAACGGCGAGGTGCTGCTGCGC 1044  
QY 400 ACCCGCGAGCAATTTGACTTNCACCAAC 429  
Db 1045 TTCCGCCCGCCTACGGCTTCGCAACATC 1074

## RESULT 7

US-10-411-910A-257  
; Sequence 257, Application US/10411910A  
; Publication No. US20040209256A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillion, Harrison F.  
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes  
; CURRENT APPLICATION NUMBER: US/10/411,910A  
; CURRENT FILING DATE: 2003-04-12  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 257  
; LENGTH: 1389  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-10-411-910A-257

Query Match 7.8%; Score 46.6; DB 8; Length 1389;  
Best Local Similarity 44.9%; Pred. No. 0.00065;  
Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;  
QY 40 GCGGAAGCGGATGCGGGCGAAGAGCTGTTGATGACCTGGCGCGCAGAGGCGANG 99  
Db 685 GTGTTGTTGGCCCTCTCTACGACAGAGCTGGAGGCCCTGGCGAGGGCTGAGCAC 744  
QY 100 AAGTGGCGGTGACACCTTCTAGGATGAGTGTGCTGCTGACCGGAGCTGCTGCCCTTC 159  
Db 745 ACCGTGAACCGCGCCCGCGACCGACTGCTGCTGACGAGCGCGGAGATCGCCCAATC 804  
QY 160 TTGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTG 219  
Db 805 ATGAGCAGAGCGACCTGAGCGTGAAGACATCGCCGTGACACCTTTCGGGCAATG 864  
QY 220 TTTGGCGGAGCAGACCAATATCAAGGGCCGAAGCATGTACGACGACACGCCCCATCTGGTC 279  
Db 865 AAGGAGGTGGCGTGCAGCGCCACGACGCGGTGAGCAGCGACGCGCCACCTGGCCACGTG 924  
QY 280 AAGGGCCACGGCTGGACCGCCACCGCCACTTTGACAGATCAAGCAGTACCTTGGAGACG 339  
Db 925 TTCCGCCACGCGCCCAAGGAGCTTTCGCGGAGCAGCTGGAGGAGATCACCTACCGCGCC 984  
QY 340 CTGCAAGAGATGGCGCTCAGCAGGATGTATCCAGCAGCGCGCGGAGTGGTGGATCC 399  
Db 985 CTGCGCAACAGGACTTCCACGAGGTGACCTCGAAGAAACGGCGAGGTGCTGCTGCGC 1044  
QY 400 ACCCGCGAGCAATTTGACTTNCACCAAC 429  
Db 1045 TTCCGCCCGCCTACGGCTTCGCAACATC 1074

## RESULT 8

US-10-369-493-32038  
; Sequence 32038, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 32038  
; LENGTH: 1209  
; TYPE: DNA  
; ORGANISM: Thermobifida fusca  
; US-10-369-493-32038

Query Match 7.7%; Score 46.2; DB 6; Length 1209;  
Best Local Similarity 55.2%; Pred. No. 0.00083;  
Matches 90; Conservative 0; Mismatches 73; Indels 0; Gaps 0;  
QY 248 GAAGCATGTACGACGACACGCCCATCTGCTCAAGGGCCACGCGCTGGACCACCGCACT 307  
Db 86 GCACCCCTGCTCTTCGACGAAGTGTCTGGTGGAGCGCGCCCGGAGGAGCAGCAGCTGT 145  
QY 308 TTGACAAAGATCAAGCAGTACCTTGGAGACACGCTGCAAGAGATGGCGGTCAACAGATG 367  
Db 146 TCGTCCAGCTCTGCGGGACCGGGGGGTGACCGTGCATGAATTCGCGACGCTCTCGCG 205  
QY 368 TGATCCAGCAGCGCGCGGAGTGGTGGAGTGCACCCGCGACGA 410  
Db 206 AGACTCTGCATCCCCGAGGCGAAGAGTTTATCTCCACGA 248

## RESULT 9

US-10-411-910A-264  
; Sequence 264, Application US/10411910A  
; Publication No. US20040209256A1  
; GENERAL INFORMATION:  
; APPLICANT: Dillion, Harrison F.  
; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes  
; FILE REFERENCE: H2041203-P  
; CURRENT APPLICATION NUMBER: US/10/411,910A  
; CURRENT FILING DATE: 2003-04-12  
; NUMBER OF SEQ ID NOS: 343  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 264  
; LENGTH: 1509  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-411-910A-264

Query Match 7.7%; Score 46.2; DB 8; Length 1509;  
Best Local Similarity 46.2%; Pred. No. 0.00089;  
Matches 153; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
QY 54 CGGCGCGCAAGAAGCTGTTGATGACCTGGCGCGCAGAGGATGAAGTGGCGGTGA 113  
Db 846 CGGCGCGCAGCGCTTCGAGCGCGCAAGATCGCCCCCTGCACAGACGCTGGCGCGCG 905  
QY 114 CACCTTCTAGATAAGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCAGTCCCTGGA 173  
Db 906 CGGCGAGATCGCCCGATCATGAGCAGGCGGCGACCTGAGCGTGGCGACCGCCGCTGGA 965  
QY 174 CATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCTGTTTGGCGGAGCAGA 233  
Db 966 CACCTGTTTCGGGCACTTGAAGGAGACAGGTGACCCGCCACGACGCGCGCAGCAGCA 1025  
QY 234 CCAATACAGGGCGCGAAGCATGTACGACGACACGCCCATCTGCTCAAGGGCCACCGCCT 293  
Db 1026 CGGCGACCTGCGCCACATCTTCGCGCACCGCGCAAGAGCTGTTCAACAGGAGCTGGA 1085  
QY 294 GGACACCGCCACTTTGACAAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGG 353  
Db 1086 GGAGGTGACCTACCGCGCCCTGCGCAACAGAGACTTCCAGGAGGTGACCTGGAGAGAA 1145

QY 354 CGTCACGAGGATGTCATCCAGCACGCCGCC 384  
Db 1146 CGCGGAGGTGCTGCTCGCTTCGCCGCCGCC 1176

## RESULT 10

US-10-437-963-69229  
; Sequence 69229, Application US/10437963  
; Publication No. US20040123343A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 69229

; LENGTH: 2209

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_69918C.1  
US-10-437-963-69229

Query Match 7.7%; Score 45.8; DB 7; Length 2209;

Best Local Similarity 46.1%; Pred. No. 0.0013;

Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 110 TTGACACCTTCTACGATAGTCTGGTGTGACCGGAGCTGTGCGCTTCTTCAGTCCG 169  
Db 400 TCAGTACGTGTGCTCAAGAGGACGACGACGAGCTCCCGAAGCTCCCGACGACCTGTGCGGG 459  
QY 170 TGGACATCAAGAGGAGAGATCAAGCAGTCAAGTTCATGACTTCGTGTTGGGGAG 229  
Db 460 AGATCATCAGCGGACAGAGTCTGGGGTGGAGGAGTACAGTTCCTCTCAAGGTCA 519  
QY 230 CAGACCAATACAGGGCGGAGCATGTACGACACACGCCCCTCTGGTCAAGGGCCACG 289  
Db 520 TCGTCACTCCGATCGGCGAGGACCTACGGGCCCGGACATCATCGCGGGCGG 579  
QY 290 GCTGGACCAACCGCCACTTTGACAGATCAAGCAGTACCTTTGGAGAGAGCTGCAAGAGA 349  
Db 580 ACGCCGCCCGGACCGCTCGCGGGGATGGAGGAGATGGACGAGAGCTTCCACGCCG 639  
QY 350 TGGGCTCAAGAGGATGTATCAGCAGCGCCCGGAGTGGTGGAGTCCACCGCGAGC 409  
Db 640 TCGTCAAGAGTGTTCGCGCGCTCGTCCGCGCGCGCGCGCGCGCGCGCGCGCG 699  
QY 410 AATTGACTTCCCAACAACTGGCGACCCA 439  
Db 700 ACCTCGACCTCTCTGCTGCTCAAGTGTCCA 729

## RESULT 11

US-10-437-963-97363/c

; Sequence 97363, Application US/10437963

; Publication No. US20040123343A1

## GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 97363

; LENGTH: 2238

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95374C.1  
US-10-437-963-97363

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 97363  
; LENGTH: 2238  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95374C.1  
US-10-437-963-97363

Query Match 7.6%; Score 45.2; DB 7; Length 2238;

Best Local Similarity 50.2%; Pred. No. 0.0021;

Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 216 CTGTTTGGCGGAGGAGACCAATACAGGGCGGAGCATGTACGAGCAGACAGCCCATCT 275  
Db 1249 CGTGTTCGCGGCTGCGAGCGCGCTCGCGCGCGCATCTTCGTGACCTCGCCGCTG 1190  
QY 276 GGTCAAGGGCCAGCGCTGGACACCGCATCTTGCACAGATCAAGCAGTACCTTGAGA 335  
Db 1189 CGCCATGTCTCAGATGCTCACTTACCAGGCGCTGCGCATGACGAAGCGCGCCCGA 1130  
QY 336 GACGCTGCAAGAGATGGCGCTCAAGCAGGATGTATCCAGCAGCGCGCGGAGTGGTGA 395  
Db 1129 GAAGCTCTTCAAGGTGCTGACATGTACGAGCGCGCTCCCGAGCGCGCGCGTCAATCGA 1070  
QY 396 GTCCACCGCGGAGCAATTTGACTTNCCTCCCAACAACTGCGC 434  
Db 1069 CGCTTATCGCGCTGTCTCCACCACGACGCGCGCGC 1031

## RESULT 12

US-10-502-351-1

; Sequence 1, Application US/10502351

; Publication No. US20050155088A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Lian Hui

; APPLICANT: Xu, Jin Liang

; TITLE OF INVENTION: Ralstonia AHL-Acylase Gene

; FILE REFERENCE: 2977-154

; CURRENT APPLICATION NUMBER: US/10/502,351

; CURRENT FILING DATE: 2004-07-23

; PRIOR APPLICATION NUMBER: PCT/SG02/000011

; PRIOR FILING DATE: 2002-01-23

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1

; LENGTH: 3743

; TYPE: DNA

; ORGANISM: Ralstonia sp.

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (16)..(16)

; OTHER INFORMATION: n is a, c, g, or t

US-10-502-351-1

Query Match 7.6%; Score 45.2; DB 9; Length 3743;

Best Local Similarity 45.2%; Pred. No. 0.0024;

Matches 164; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 69 GTTGTGATGACCTGGCGGCGCAGAGGATGAAGTGGCGGTGACACCTTTACGATAA 128  
Db 2055 GCTCGAGGTGATGGCGGCTCGATCGCGGCTTCCCGGTGGTGGAGCATCGGCTTCAACAA 2114  
QY 129 GGTGTGCTGACCGCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGACAGAA 188  
Db 2115 GGACGTGGGTGGAGCGCACACCGTCTCCACCGCGCGCGCTTTCACCTTGTTCGAATGAA 2174

QY 189 GATGAAGCAGTCAAGTTATGAGTTCGTTGGCGGAGCAGACCAATACAAAGGCGG 248  
| | | | |  
Db 2175 GCTGGCGGAGGCGACCCGACCACTTACCTGTCGAGCGGACGCCGCAAGATGACCA 2234  
| | | | |  
QY 249 AAGCATGTACGACGACACGCCCATCTGTGTCAGAGGCCACGGCTTGAGACACCGCCACTT 308  
| | | | |  
Db 2235 CGCAACGGTCCGCTTCGACGTCAAGCTGCCGAGCGCGCTCGAGCGCGCACGACAC 2294  
| | | | |  
QY 309 TGACAAGATCAACGAGTACCTTGAGAGAGCGCTGCAAGAGATGGCGTCAAGCAGATGT 368  
| | | | |  
Db 2295 CTTCTACGACCAACCATCTACGCGCCGCTGCTGTCGATGCCGAGCGCGCATGCCGCTGGAC 2354  
| | | | |  
QY 369 GATCCAGACGCGCGGAGTGTGAGTCCACCCGCGAGCAATTTGACTTNNCCCAACAA 428  
| | | | |  
Db 2355 CACGCAAGAGGCTACGCCCTGCGGAGCGGCAACCGCAACACGCGCTCGGTGCAGAG 2414  
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QY 429 CTG 431  
| | | | |  
Db 2415 CTG 2417  
| | | | |

RESULT 13  
US-10-437-963-35783  
; Sequence 35783, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; PRIOR FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 35783  
; LENGTH: 1445  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_39672C.1  
US-10-437-963-35783

Query Match 7.4%; Score 44.4; DB 7; Length 1445;  
Best Local Similarity 46.5%; Pred. No. 0.0033;  
Matches 141; Conservative 0; Mismatches 162; Indels 0; Gaps 0;  
QY 139 GACCCGAGCTGCTCCCTTCTTCGAGTCCCTGACATGCAAGAGCAGAGATGAAGCAG 198  
| | | | |  
Db 167 GACGCTCGAGCTGGCGGAGCAGCTCGACGGAGCTCGCGAGCTCGAGCCCAAGCTG 226  
| | | | |  
QY 199 GTCAGTTATGAGTCTGTTGTTGGCGAGCAGACCAATACAAAGGCCGCAAGATGTAC 258  
| | | | |  
Db 227 GCCAGCTGGCGCGCGGCAACCCCGGCGTCTCCAGGTGCACGCGGTGTACGAGGAC 286  
| | | | |  
QY 259 GAGCACAACCCCATCTGTCAGGGCGCAGCGCTGACACCCGCACTTTGACAGATC 318  
| | | | |  
Db 287 GACGCTGGAGCGACATGGTGTATGACCTCTGCTCCGGCCCCGACCTGCTCGACTGGATC 346  
| | | | |  
QY 319 AAGCAGTACCTTGAGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGCAC 378  
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Db 347 CGCTTCGCGCGGCGCGCGCTCCCGAGCGCGCTCGCCCGCGCTCGTCGCGAGCTC 406  
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QY 379 GCGCGCGGAGTGTGAGTCCACCCGCGAGCAATTTGACTTNNCCCAACAACTGGGCAACC 438  
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Db 407 GCGGAGGCGCTCGCGCACTGCGCACCGCGGGGTCCGCCACCGCGAGCTCAAGCGCCGAC 466  
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QY 439 AAC 441  
| | | | |  
Db 467 AAC 469  
| | | | |  
RESULT 14  
US-10-389-566-49/c  
; Sequence 49, Application US/10389566  
; Publication No. US20040025202A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Technology, LLC  
; APPLICANT: Laurie, Cathy C  
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants  
; FILE REFERENCE: 38-77(52900)D  
; CURRENT APPLICATION NUMBER: US/10/389,566  
; CURRENT FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US 60/365,301  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/391,786  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/392,018  
; PRIOR FILING DATE: 2002-06-26  
; NUMBER OF SEQ ID NOS: 2459  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 49  
; LENGTH: 1000  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-389-566-49  
Query Match 7.4%; Score 44.2; DB 7; Length 1000;  
Best Local Similarity 53.8%; Pred. No. 0.0034;  
Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;  
QY 66 GCTGTTTATGACCTGGGGCGGCGAGAGCATGAAGCTGGCGGTGACACCTTCTACGA 125  
| | | | |  
Db 676 GCAGTTTATCGCGCGGTCTCACGCCGCGGAGATGCTCACGGTAGAGGGCTTACCACGA 617  
| | | | |  
QY 126 TAAGTGTCTGCTGACCGGAGCTGCTCCCTTCTTCGAGTCCCTCGACATGCAAGAGCA 185  
| | | | |  
Db 616 CATGCTGCTGCGCGAGCGGCAAGCGCTGCCCGCGCGAGATCCTGGGTTGCAACGCCCC 557  
| | | | |  
QY 186 GAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTTTGGCGGAGCAGAC 234  
| | | | |  
Db 556 GACGCTCAAGAGTCGAGGAGTGGCGCGCTGGTTCGTCGCCGAC 508  
| | | | |  
RESULT 15  
US-10-369-493-39791  
; Sequence 39791, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 39791  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Xanthomonas campestris  
US-10-369-493-39791  
Query Match 7.4%; Score 44.2; DB 6; Length 1377;  
Best Local Similarity 48.2%; Pred. No. 0.0037;

Matches: 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY	151	CTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATG	210
Db	784		
QY	211	AGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGGCGGAAGCATGTACGACGCACAGCC	270
Db	844		
QY	271	CATCTGCTCAAGGGCCACGGCCTGGACCCACCGCCACTTTGACAAAGATCAAGCAGTACCTT	330
Db	904		
QY	331	GGAGAGCAGTGTCAAGAGATGGCGCGTCAAGCAGGATGTGATCCAGCACCGCCCGGAGTG	390
Db	964		
QY	391	GTGGAGTCCACCCGCA	407
Db	1024		
		GTGGTGGCGCTGGCGCA	1040

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Job time : 754 secs

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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 19:29:58 ; Search time 431 Seconds  
(without alignments)  
2958.597 Million cell updates/sec

Title: US-09-920-953-2  
Perfect score: 597  
Sequence: 1 ggcgtgcctgcagacgcgcg.....agccatttcgcaccaagc 598

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New.\*  
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2: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
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8: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
9: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
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11: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
12: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
13: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	7.0	1280	12	US-11-219-995-4
2	40.8	6.8	1134	8	US-10-517-939-295
3	37.8	6.3	1027	12	US-11-136-527-94
4	37	6.2	859	7	US-10-714-887-161
5	37	6.2	1222	12	US-11-136-527-3173
6	36.8	6.2	7474	12	US-11-069-834-49
7	36.6	6.1	2644	12	US-11-136-527-2717
8	36.4	6.1	581	6	US-09-925-065A-662231
9	36.4	6.1	619	12	US-11-136-527-3549
10	36.4	6.1	619	12	US-11-136-527-7645
11	36.2	6.1	1400	12	US-11-136-527-4371
12	36.2	6.1	3624	7	US-10-755-092-6
13	36.2	6.1	4509	12	US-11-087-100-5
14	36.2	6.1	4509	12	US-11-087-084-5
15	36.2	6.1	4509	12	US-11-087-085-5
16	36.2	6.1	5941	12	US-11-136-527-275
17	35.2	5.9	600	12	US-11-136-527-5577
18	35.2	5.9	658	12	US-11-136-527-1481
19	35.2	5.9	1488	12	US-11-219-995-3
20	35.2	5.9	1642	6	US-09-925-065A-552370

21	35.2	5.9	2534	12	US-11-219-995-1	Sequence 1, Appli
22	35.2	5.9	4457	8	US-10-775-163-259	Sequence 259, App
c	35	5.9	486	6	US-09-925-065A-751390	Sequence 751390,
23	35	5.9	902	12	US-11-156-003-7	Sequence 7, Appli
24	35	5.9	1400	12	US-11-136-527-4370	Sequence 4370, Ap
25	35	5.9	1611	12	US-11-156-003-21	Sequence 21, Appl
26	35	5.9	1611	12	US-11-156-003-22	Sequence 22, Appl
27	35	5.9	1629	12	US-11-156-003-4	Sequence 4, Appli
28	35	5.9	1629	12	US-11-156-003-17	Sequence 17, Appl
29	35	5.9	1629	12	US-11-156-003-18	Sequence 18, Appl
30	35	5.9	1629	12	US-11-156-003-19	Sequence 19, Appl
31	35	5.9	1629	12	US-11-156-003-20	Sequence 20, Appl
32	35	5.9	1650	12	US-11-156-003-6	Sequence 6, Appli
33	35	5.9	2010	8	US-10-821-234-248	Sequence 248, App
34	35	5.9	6021	12	US-11-136-527-274	Sequence 274, App
35	35	5.9	1615	6	US-09-925-065A-43408	Sequence 43408, A
36	34.8	5.8	1635	6	US-09-925-065A-554906	Sequence 554906,
37	34.8	5.8	600	12	US-11-128-061-4054	Sequence 4054, Ap
38	34.6	5.8	600	12	US-11-128-049-4054	Sequence 412, App
39	34.6	5.8	1155	12	US-11-128-061-412	Sequence 412, App
40	34.6	5.8	1155	12	US-11-128-049-412	Sequence 5041, Ap
41	34.6	5.8	1400	12	US-11-136-527-5041	Sequence 945, App
42	34.6	5.8	2230	12	US-11-136-527-945	Sequence 1418, Ap
43	34.4	5.8	1792	9	US-11-072-512-1418	Sequence 8, Appli
44	34.4	5.8	2130	12	US-11-165-067A-8	
45	34.4	5.8				

ALIGNMENTS

RESULT 1  
US-11-219-995-4  
; Publication US/11219995  
; Publication No. US2006003379A1  
; GENERAL INFORMATION:  
; APPLICANT: Miyazono, Kohei  
; APPLICANT: Kawabata, Masahiro  
; TITLE OF INVENTION: SMAD6 AND USES THEREOF  
; FILE REFERENCE: L0461.70148US01  
; CURRENT APPLICATION NUMBER: US/11/219,995  
; CURRENT FILING DATE: 2005-09-06  
; PRIOR APPLICATION NUMBER: US 10/390,553  
; PRIOR FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: US 09/923,922  
; PRIOR FILING DATE: 2001-08-07  
; PRIOR APPLICATION NUMBER: US 09/096,776  
; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: US 60/049,990  
; PRIOR FILING DATE: 1997-06-13  
; PRIOR APPLICATION NUMBER: US 60/053,040  
; PRIOR FILING DATE: 1997-07-18  
; PRIOR APPLICATION NUMBER: US 60/066,173  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 1280  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-219-995-4

Query Match	7.0%;	Score 41.6;	DB 12;	Length 1280;
Best Local Similarity	52.7%;	Pred. No. 0.044;		
Matches	89;	Conservative	0;	Mismatches 80;
Indels	0;	Gaps	0;	
QY	266	ACGCCCATCTGGTCAAGGCGCGCTGACACCGCCACTTTGACAGATCAAGAGT	335	
Db	405	ACCTACTCAGGCGACGGCTTCTGCTGGCGCAGCTCAACCTGGAGCAGCGAGT	454	
QY	326	ACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGCAGCGCGC	385	
Db	465	CGGTGCGGGAACGCGCGCAAGATCGGCTTCGGCTTCCTGCTCAGCAAGAGCGCCGACG	524	



PRIOR APPLICATION NUMBER: 09/394,519  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: 09/533,392  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,029  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/532,591  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 09/533,030  
PRIOR FILING DATE: 2000-03-22  
PRIOR APPLICATION NUMBER: 60/125,814  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: 09/713,994  
PRIOR FILING DATE: 2000-11-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 430  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 161  
LENGTH: 859  
TYPE: DNA  
ORGANISM: *Triticum aestivum*  
FEATURE:  
OTHER INFORMATION: G3736 Predicted polypeptide sequence is orthologous to G1792  
US-10-714-887-161

Query Match 6.2%; Score 37; DB 7; Length 859;  
Best Local Similarity 50.6%; Pred. No. 0.83;  
Matches 88; Conservative 0; Mismatches 86; Indels 0; Gaps 0;  
QY 257 ACGACGACACGCCCATCTGTTCAAGGCGCCACGCGCTGGACACCGCCACTTTGACAAGA 316  
DB 350 ACCGGCGCGACGCTACGAGGCGCGCCAGCGCGCCAGGCGCTTCTGTCGCG 409  
QY 317 TCAAGCAGTACCTTGCAGAGACGCTGCAAGAGATGGCGGTCAAGCAGGATGTGATCCAGC 376  
DB 410 CGAGGACGACAGATCAGCAGCAGCAGCAGGCGGAGGCGGTGATCGAGTTCGAGTACC 469  
QY 377 ACGCCCGCGAGTGGTGGAGTCCACCGCGACGAATTTGACTTNCACCAACT 430  
DB 470 TGGACGACGACGCTGCTGCAGTCCATGCTCCACGACCAACCAACTCAACAGT 523

RESULT 5  
US-11-136-527-3173  
Sequence 3173, Application US/11136527  
Publication No. US20050287570A1  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136,527  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3173  
LENGTH: 1222  
TYPE: DNA  
ORGANISM: *Rattus norvegicus*  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (673)..(673)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (802)..(802)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (910)..(910)  
OTHER INFORMATION: n is a, c, g, or t

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (912)..(912)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (925)..(925)  
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NAME/KEY: misc feature  
LOCATION: (1063)..(1063)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1074)..(1074)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1077)..(1077)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1080)..(1080)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-136-527-3173

Query Match 6.2%; Score 37; DB 12; Length 1222;  
Best Local Similarity 50.3%; Pred. No. 0.89;  
Matches 91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;  
QY 14 ACGCGCCACGACGACGAGAGCGGGAAGCGGATCGCGGCGCAGAGAGCTGTTTG 73  
DB 196 AGGAGCGCTTCAACATGATTGATCAGAACCGTGCTTCATTGACAAGGAGGACCTAC 255  
QY 74 ATGACTGGCGCGCGCAGAGGACATGAGCTGCGGTTTCACACCTTCTACGATAAGGTGC 133  
DB 256 ATGATGCTGCGCTCCCTCGGGAAGAACCCACGATGAGTACCTGGAGGGTATGATGA 315  
QY 134 TGGCTGACCGGAGCTGTGCGCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAGATGA 193  
DB 316 ACGAGCGCGCGGACCTATCACTTCACCATGTCTCTACTATGTTTGGGAGAAGCTGA 375  
QY 194 A 194  
DB 376 A 376

RESULT 6  
US-11-069-834-49  
Sequence 49, Application US/11069834  
Publication No. US20050276811A1  
GENERAL INFORMATION:  
APPLICANT: CARROLL, MICHAEL C.  
APPLICANT: MOORE JR., FRANCIS D.  
APPLICANT: HECHTMAN, HERBERT B.  
TITLE OF INVENTION: NATURAL IGM ANTIBODIES AND INHIBITORS THEREOF  
FILE REFERENCE: CRA-002.01  
CURRENT APPLICATION NUMBER: US/11/069,834  
CURRENT FILING DATE: 2005-03-01  
PRIOR APPLICATION NUMBER: 60/588,648  
PRIOR FILING DATE: 2004-07-16  
PRIOR APPLICATION NUMBER: 60/549,123  
PRIOR FILING DATE: 2004-03-01  
NUMBER OF SEQ ID NOS: 65  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 49  
LENGTH: 7474  
TYPE: DNA  
ORGANISM: *Homo sapiens*  
US-11-069-834-49  
Query Match 6.2%; Score 36.8; DB 12; Length 7474;  
Best Local Similarity 46.1%; Pred. No. 1.4;

Matches	165;	Conservative	0;	Mismatches	187;	Indels	6;	Gaps	1;
QY	65	AGCTGTTTGATGACCTGGGGCGGCAGAAAGCATGAAGCTGGCGGTTTGACACCTTTCTACG	124						
Db	4812	AGCTGGAGGACGAGCTCAGGCGCACACCGAAGATGCAAGCTTCGCGTTGGAGGTCAACCTGC	4871						
QY	125	ATAAGGTGCTGGCTGACCCGGAGCTGTCGCCCTTCTTCGAGTCCCTGGACATGCACAGAC	184						
Db	4872	AGGCCATGAAGGCCCGAGTTTCAGCGGGACCTGCAAGGCGCGGACGACGAGCGAGGAGA	4931						
QY	185	AGAAGATGAAGCAGGTCACAGTTTCATGAGCTTTCGTGTTTGGCGGAGCAGACCAATACAAGG	244						
Db	4932	AGAAGAAGCAGCTGGTCAGACAGCTGCGGAGATGGAGGCGAGAGCTGGAGACGAGAGGA	4991						
QY	245	GCCGAGATGTTAGAGCGACACGCCCATCTGGTCAAGGGCCACGGCTTGGACCAACC---	301						
Db	4992	AGCAGCGCTCGATGGCAGTGGCGGCGCGCCCGGGAAGCTTGGAGATGGACCTGAAAGCACCTG	5051						
QY	302	---GCCACTTTGACAAGCATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGGCGTCA	358						
Db	5052	AGGGGCACATCGACTCGGCCAACAGAAACCGGAGCAGAGCCATCAACACAGCTGCGGAAGC	5111						
QY	359	AGCAGGATGTGATCCAGCACCGCCCGGAGTGFTGGAGTCCACCCGCGACGAATTGA	416						
Db	5112	TGCAGGCCAGATGAAGGATGCTGATGCGCGAGCTGGATGATCACCCGGCGCTCTCGTGA	5169						

RESULT 7

US-11-136-527-2717

; Sequence 2717, Application US/11136527

; Publication No. US20050287570A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

; FILE REFERENCE: 031896-041000 (AM101086)

; CURRENT APPLICATION NUMBER: US/11/136,527

; PRIORITY FILING DATE: 2005-05-25

; PRIOR APPLICATION NUMBER: US 60/574,294

; NUMBER OF SEQ ID NOS: 362830

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2717

; LENGTH: 2644

; TYPE: DNA

; ORGANISM: Rattus norvegicus

US-11-136-527-2717

```

; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 662231
; LENGTH: 581
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-662231

Query Match      6.1%; Score 36.4; DB 6; Length 581;
Best Local Similarity 47.7%; Pred. No. 1.1;
Matches 103; Conservative 1; Mismatches 112; Indels 0; Gaps 0;

Qy      178  CAAGAGCAGAGAAGATGAAGCAGAGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAA 237
Db      251  CCAGCGCACCCGACGAGCGCCGCGAGCTGTCGCGGCATGTTCCAGGCGGCGCAGCGC 192
Qy      238  TACAAGGGCCGAGAGCATGTTACGACGACACACGCCCATCTGCTCAAGGGCCACGGCCTTGAC 297
Db      191  CCCCAGGAGTGGGCCCATGTGAGGGCCCCCGCGACGGGCTGAAGAGGAGCAGCGCTACTGGAY 132
Qy      298  CACGCCCATCTTGACAAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGGTC 357
Db      131  GACCGCCACACAGCGGCGCTGGACTCCATGAAGACGAGGAGTACGAGCAGATGCTCAAG 72
Qy      358  AAGCAGGATGTGATCCAGCACGCCGCCGCGAGTGGTG 393
Db      71  GAGCTTGAGGAGATCCGCCTCGAGCCCGCAGGAGGTG 36

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Db 11 GCCATGATGCGGAGGAGCTGAAGAGGAGCAGGACACACGAGCCCATCTGGAGCGGATG 70  
QY 232 GACCAATACAAAGGCGGAGCATGTACGAGCAGCAGCCCATCTGTCAAGGGCCACGGC 291  
Db 71 AAGAAGAACCTCGAGCAGACAGTGAAGGACCTGCAGCAGCCGTCTGGACGAGGCTGAGCAG 130  
QY 292 CTGGACACCGCCACCTTTGACAAGATCAAGCAGTACCTTGGAGAGCGCTGCAAGAGATG 351  
Db 131 CTGGCCCTGAAGGCTGCAAGAGCAGATCCAGAACTGGAGCCAGGGTGCGGGAGTTG 190  
QY 352 GCGGTCAAGCAGGATGTGATCCAGCA 377  
Db 191 GAAAGCAGCTGGATGCAGAGCAGAA 216

## RESULT 10

US-11-136-527-7645  
; Sequence 7645, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7645  
; LENGTH: 619  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-7645

Query Match 6.1%; Score 36.4; DB 12; Length 619;  
Best Local Similarity 48.5%; Pred. No. 1.1;  
Matches 100; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
QY 172 GACATGCAAGCAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCA 231  
Db 11 GCCATGATGCGGAGAGCTGAAGAGGAGCAGGACACACGAGCCCATCTGGAGCGGATG 70  
QY 232 GACCAATACAAAGGCGGAGCATGTACGAGCAGCAGCCCATCTGTCAAGGGCCACGGC 291  
Db 71 AAGAAGAACCTCGAGCAGACAGTGAAGGACCTGCAGCAGCCGTCTGGACGAGGCTGAGCAG 130  
QY 292 CTGGACACCGCCACCTTTGACAAGATCAAGCAGTACCTTGGAGAGCGCTGCAAGAGATG 351  
Db 131 CTGGCCCTGAAGGCTGCAAGAGCAGATCCAGAACTGGAGCCAGGGTGCGGGAGTTG 190  
QY 352 GCGGTCAAGCAGGATGTGATCCAGCA 377  
Db 191 GAAAGCAGCTGGATGCAGAGCAGAA 216

## RESULT 11

US-11-136-527-4371  
; Sequence 4371, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4371

LENGTH: 1400  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-11-136-527-4371  
Query Match 6.1%; Score 36.2; DB 12; Length 1400;  
Best Local Similarity 40.4%; Pred. No. 1.5;  
Matches 86; Conservative 22; Mismatches 105; Indels 0; Gaps 0;  
QY 169 CTGGCATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGA 228  
Db 15 CTGGGKCAASKGGAARARYRTSCAGGAGCTGGAGAGRTCCKMWRGCMWYTKGWSGW 74  
QY 229 GCAGACCAATACAAAGGCGGAGCATGTACGAGGAGCAGCCCATCTGTCAAGGGCCAC 288  
Db 75 GRGWMGCKGSRGCGCAGTCAGCCCTTGAAGAGGCTGAGGCGCTCYCTGGAGCATGAGGAG 134  
QY 289 GGCCTGGACACCGCCACCTTTCAGCAAGATCAAGCAGTACCTTGGAGAGAGCGCTGCAAGAG 348  
Db 135 GCGAAGATCTCCGAGCCGAGCTGGAGTTCAACCAATYAAGCAGAGATCGAAGAG 194  
QY 349 ATGGGCGTCAAGCAGGATGTGATCCAGCAGCGC 381  
Db 195 CTGGCAGAGAGCAGGAGATGGAGCARGSC 227

## RESULT 12

US-10-755-092-6  
; Sequence 6, Application US/10755092  
; Publication No. US20060021095A1  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Evola, Stephen V.  
; Crossland, Lyle D.  
; Wright, Martha S.  
; Merlin, Ellis J.  
; Launis, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/755,092  
FILING DATE: 08-Jan-2004  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-Nov-2001  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy

```
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3624 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Synthetic DNA"
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3621
; OTHER INFORMATION: /product= "Full-length, maize
; optimized cry1B"
; /note= "Disclosed in Figure 6."
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-755-092-6

Query Match 6.1%; Score 36.2; DB 7; Length 3624;
Best Local Similarity 44.4%; Pred. No. 1.9;
Matches 146; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 78 CTTGGGGCGGCGAGAGGATGAAGCTGGGGTGTGACACTTCTTACGATGAAGTGTGGC 137
Db 2811 CGTGGACAGCGAGTACGACCGCTTGCAGCGCCGACCAACATCGGCATGATCCACGCCG 2870

QY 138 TGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGAGCAGAGATGAAGCA 197
Db 2871 CGAAGCTGGTGACCGCATCCGCGAGGCTTCTTGGAGGAGCTGCCCTGTATCCCGG 2930

QY 198 GGTCAAGTTCATGAGTCTGTGTTGGCGGAGCAGACCAATCAAGGGCGCGAAGCATGTA 257
Db 2931 CGTGAAGCGCGAGATCTTCGAGGAGCTGGAGGCCACATCATCACCGCCATCAGCTGTA 2990

QY 258 CGACGCACAGCCCATCTGTCAAGGGCCACGGCTGGACACCGCCACTTTGACAGAT 317
Db 2991 CGACGCCGGAACGTGTGGAAGAACGGCGACTTCAACACGGGCTGACCTGTCTGGAACGT 3050

QY 318 CAAGCATACCTTGGAGAGCGCTGCAAGATGGCGTCAAGCAGGATGTGATCCAGCA 377
Db 3051 GAAGGGCCAGCTGACGTGAGCAGAGACCCACCGCAGCGACCTGGTGATCCCGGAGTG 3110

QY 378 CGCGCGCGAGTGTGTGAGTCCACCCCGC 406
Db 3111 GGAGGCGGAGTGAGCCAGGCGGTGCGG 3139

RESULT 13
US-11-087-100-5
; Sequence 5, Application US/11087100
; Publication No. US2005026640A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE REFERENCE: 2997-29
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-084-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCATCTGGTCAAGGGCCACGGCTGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAGGTCCGTGCGCGCCCAATCTCCCGCACAGGGCAAGCTCG 1129

QY 326 ACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGACGCCCGC 385
Db 1130 TCTACGTGATGAGATCAAGGAGTGGCTTCGACGAGGACAAAGCCCTTAGCCTCGAC 1189

RESULT 14
US-11-087-084-5
; Sequence 5, Application US/11087084
; Publication No. US20050273883A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE REFERENCE: 2997-29
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-084-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCATCTGGTCAAGGGCCACGGCTGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAGGTCCGTGCGCGCCCAATCTCCCGCACAGGGCAAGCTCG 1129

QY 326 ACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGACGCCCGC 385
Db 1130 TCTACGTGATGAGATCAAGGAGTGGCTTCGACGAGGACAAAGCCCTTAGCCTCGAC 1189
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; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-100-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCATCTGGTCAAGGGCCACGGCTGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAGGTCCGTGCGCGCCCAATCTCCCGCACAGGGCAAGCTCG 1129

QY 326 ACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGACGCCCGC 385
Db 1130 TCTACGTGATGAGATCAAGGAGTGGCTTCGACGAGGACAAAGCCCTTAGCCTCGAC 1189

QY 386 GAGTGTGGAGTCCACCCCGCAGCAATTTGACTTNCACCAACTGCGCACCCCACTG 443
Db 1190 CCGACGTCAACATCATTTGATGTGACTTCGAAAAGGGCCAGGACTTTAGCCTCGAC 1247
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RESULT 14
US-11-087-084-5
; Sequence 5, Application US/11087084
; Publication No. US20050273883A1
; GENERAL INFORMATION:
; APPLICANT: Metz, James
; APPLICANT: Barclay, William
; APPLICANT: Platt, James
; APPLICANT: Kuner, Jerry
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORFA of a PUFA Polyketide Synthase
; FILE REFERENCE: 2997-29
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: 09/231,899
; PRIOR FILING DATE: 1999-01-14
; PRIOR APPLICATION NUMBER: 60/284,066
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: 60/298,796
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/323,269
; PRIOR FILING DATE: 2001-09-18
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 5
; LENGTH: 4509
; TYPE: DNA
; ORGANISM: Schizochytrium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(4509)
; US-11-087-084-5
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Query Match 6.1%; Score 36.2; DB 12; Length 4509;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 266 ACGCCATCTGGTCAAGGGCCACGGCTGACCAACCGCCACTTTGACAAGATCAAGCAGT 325
Db 1070 ACGGCCACCCCAACAGGTCCGTGCGCGCCCAATCTCCCGCACAGGGCAAGCTCG 1129

QY 326 ACCTTGGAGAGCGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGACGCCCGC 385
Db 1130 TCTACGTGATGAGATCAAGGAGTGGCTTCGACGAGGACAAAGCCCTTAGCCTCGAC 1189
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QY 386 GAGTGTGAGTCCACCGCGACGAATTGACTTNCCTCCAACTCCGCGACCCCACTG 443  
Db 1190 CCGACGTCAACATCATGTGCGACTTCGAAAAGGCCAGGACTTTAGCTCGACCG 1247

## RESULT 15

US-11-087-085-5  
; Sequence 5, Application US/11087085  
; Publication No. US20050273884A1  
; GENERAL INFORMATION:  
; APPLICANT: Metz, James  
; APPLICANT: Barclay, William  
; APPLICANT: Platt, James  
; APPLICANT: Kuner, Jerry  
; TITLE OF INVENTION: Nucleic Acid Molecule Encoding ORPA of a PUFA Polyketide Synthase  
; FILE OF INVENTION: System and Uses Thereof  
; FILE REFERENCE: 2997-29  
; CURRENT APPLICATION NUMBER: US/11/087,085  
; CURRENT FILING DATE: 2005-03-21  
; PRIOR APPLICATION NUMBER: 09/231,899  
; PRIOR FILING DATE: 1999-01-14  
; PRIOR APPLICATION NUMBER: 60/284,066  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/298,796  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/323,269  
; PRIOR FILING DATE: 2001-09-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5  
; LENGTH: 4509  
; TYPE: DNA  
; ORGANISM: Schizochytrium sp.  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(4509)  
US-11-087-085-5

Query Match 6.1%; Score 36.2; DB 12; Length 4509;  
Best Local Similarity 50.0%; Pred.No. 1.9;  
Matches 89; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 266 AGCCCATCTGTCAAGGCCACCGCGCTGGACCAACCGCCACTTTGACAAGATCAAGCACT 325  
Db 1070 ACGGCCACCCACACAGGTCCGCTGCGCGGCCAATCTCCCGCACAGGGCAAGCTCG 1129  
QY 326 ACCTTGAGAGACGCTGCAAGAGATGGCGTCAAGCAGATGTGATCCAGCAGCGCCCG 385  
Db 1130 TCTACGTCATGGAGATCAAGGAGATGGCTTCGACGAGGACCAACGACCGTACGCCATTG 1189  
QY 386 GAGTGTGAGTCCACCGCGAGATTGACTTNCCTCCAACTCCGCGACCCCACTG 443  
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Job time : 432 secs

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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 19:14:39 ; Search time 171 Seconds  
(without alignments)  
6216.268 Million cell updates/sec

Title: US-09-920-953-2  
Perfect score: 597  
Sequence: 1 GCGCTGCTGAGCGGCGG.....AGCCATTTGCGACCAAGCG 598

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
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5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
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9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97.2	16.3	381	3	US-09-902-540-5776
2	97.2	16.3	72704	3	US-09-902-540-1273
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C 4	46.4	7.8	4411529	3	US-09-103-840A-1
5	45.2	7.6	1143	3	US-09-902-540-8600
6	45.2	7.6	6821	3	US-09-902-540-907
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8	43.4	7.3	603	3	US-09-902-540-5853
9	42.8	7.2	585	3	US-09-902-540-3555
10	42.8	7.2	19019	3	US-09-902-540-1171
11	42.6	7.1	3128	3	US-09-744-072-1
12	42.4	7.1	26896	3	US-09-949-016-16800
13	42.2	7.1	759	3	US-09-252-991A-11092
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15	41.6	7.0	969	3	US-09-902-540-8164
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19	41.6	7.0	1491	3	US-09-885-722A-9
20	41.6	7.0	1524	3	US-08-840-767-3
21	41.6	7.0	1817	3	US-09-288-292A-45
22	41.6	7.0	2887	3	US-09-679-298A-1
23	41.6	7.0	3083	2	US-08-480-994-36
24	41.6	7.0	3083	2	US-08-616-844-36

ALIGNMENTS

RESULT 1  
US-09-902-540-5776  
; Sequence 5776, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5776  
; LENGTH: 381  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5776

Query Match	16.3%	Score 97.2;	DB 3;	Length 381;
Best Local Similarity	56.9%	Pred. No. 9.8e-16;		
Mismatches	199;	Conservative	0;	Mismatches 148; Indels 3; Gaps 1;
QY	61	AAGAGCTTTTGTATGACCTGGCGCGCAGAGGATGAGCTGGCGGTGACACTTC	120	
DB	19	AAGAGTGTCTACGACAGCTGGCGCGGAGAGCGCGGATGGCGCGGTGGAGGTTC	78	
QY	121	TACGATAAGTGTGCTGCTGACCGCGAGCTGCTGCGCTTCTTGAGTCCCTGGACATGCA	180	
DB	79	TACCGAGGTGCTGGCGGACCATCATACCCACTTCTTGAGGACGTGACATGGAG	138	
QY	181	GAGCAGAGATGAAGCAGCTCAAGTTCTATGAGCTTGTGTTGGCGGAGCAGACCAATAC	240	
DB	139	CGCCAGGCGCGAAGCAGAGCGTTCCTGACGATGTTGACGGTGGCGCGGTCCACTAC	198	
QY	241	AAGGCGGAGCATGTACGACCCATCTGTTCAAGGGCCACCGCTTGGACCCAC	300	
DB	199	TCGGGCAAGGACATGCGCGCGGCCACGCGCTTGTGGTGAAG---CGTGGGTGAACGAC	255	
QY	301	CGCCACTTTGACAAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCAAG	360	
DB	256	TGCATCTTCGACGGGTGGCGGCCACCTGAAGGCGACGCTGAGGAGCTGGCGGTGGCC	315	
QY	361	CAGGATGTATCCAGCACGCGCGGAGTGGTGGAGTCCACCCGCGACGA	410	

Db 316 GCGCGGCTGGCGGAGGTGATGACCATCGCGAGAGCGCCGCGCGGA 365

RESULT 2

US-09-902-540-1273  
; Sequence 1273, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1273  
; LENGTH: 72704  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)-(72704)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1273

Query Match 16.3%; Score 97.2; DB 3; Length 72704;  
Best Local Similarity 56.9%; Pred. No. 4.6e-15;  
Matches 199; Conservative 0; Mismatches 148; Indels 3; Gaps 1;  
  
Qy 61 AAGAAGCTGTTGATGACCTGGCGCGCAGAGCATGAAGCTGGCGGTGACACCTTC 120  
Db 21785 AAGAGTCTACGAGCAGCTGGCGCGAGAGCGCGCATGGCGCGGTGGAGTCTTC 21844  
  
Qy 121 TACGATAGGTGCTGGCTGACCGGAGCTGCGCTTCTTCGAGTCCCTGGACATCAA 180  
Db 21845 TACCGAAGGTGCTGGCGGACGATCACATCAGCCACTTCTTCGAGGACGTGGACATGGAG 21904  
  
Qy 181 GAGCAGAAGATGAACGAGGTCAAGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATAC 240  
Db 21905 CGCCAGCGCGCAGCAGAGAGGCGTTCTGACGATGTGAGCGGTGGCGCGTCCACTAC 21964  
  
Qy 241 AAGGCGCGAAGCATGTACGACGACAGCGCCATCTGTGTCAGGGCCACGCGCTGGACAC 300  
Db 21965 TCGGCGAAGGACATGCGCGCGGCGCAGCGCTCTGGTGAAG---CGTGGGCTGAACGAC 22021  
  
Qy 301 CGCCACTTTCACAGATCAAGCAGTACCTTGGAGAGCGCTGCAAGAGATGGGCGTCAAG 360  
Db 22022 TCGCACTTTCAGCGGTGGCGGCGCACCTGAAGCGCAGCTGGAGGAGCTGGCGGTGGCC 22081  
  
Qy 361 CAGGATGTATCCAGCAGCGCGCGGAGTGGTGAAGTCCACCCCGCAGCA 410  
Db 22082 GCGCGGCTGGTGGCGAGGTTGATACCATCGCGAGAGCGCCGCGCGGA 22131

RESULT 3

US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 7.8%; Score 46.4; DB 3; Length 4403765;  
Best Local Similarity 50.9%; Pred. No. 0.23;  
Matches 110; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
  
Qy 51 ATCGGGCGCAGAAGCTGTTGATGACCTGGCGCGGAGAGGATGAAGCTGGCGGT 110  
Db 1744933 ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGCGCATGAGGCCATCGAAGTCGTCGT 1744874  
  
Qy 111 TGACACCTTCTACGATAAGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCT 170  
Db 1744873 CGAGGACTTCTATGTTGCTGCTGCGGATGACCACTATCGGCTTCTTCAGCGGTAC 1744814  
  
Qy 171 GGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGC 230  
Db 1744813 GAACATGAGCGGCTCAAGGGCAAGCAGGTGGAGTGTTCGCGGCGCGCTTGGCGGGCC 1744754  
  
Qy 231 AGACCAATACAGGGCGGAGCATGTACGACGACA 266  
Db 1744753 CGAGCCCTATACCGGTGCGCGCATGAAGCAAGTCCA 1744718

RESULT 4

US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 7.8%; Score 46.4; DB 3; Length 4411529;  
Best Local Similarity 50.9%; Pred. No. 0.23;  
Matches 110; Conservative 0; Mismatches 106; Indels 0; Gaps 0;  
  
Qy 51 ATCGGGCGCAGAAGCTGTTGATGACCTGGCGCGGAGAGGATGAAGCTGGCGGT 110  
Db 1744808 ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGCGCATGAGGCCATCGAAGTCGTCGT 1744749  
  
Qy 111 TGACACCTTCTACGATAAGGTGCTGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCT 170  
Db 1744748 CGAGGACTTCTATGTTGCTGCTGCGGATGACCACTATCGGCTTCTTCAGCGGTAC 1744689  
  
Qy 171 GGACATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGC 230  
Db 1744688 GAACATGAGCGGCTCAAGGGCAAGCAGGTGGAGTGTTCGCGGCGCGCTTGGCGGGCC 1744629  
  
Qy 231 AGACCAATACAGGGCGGAGCATGTACGACGACA 266



Db 541 GCTCAACCCCGGAGCTGTCTACCGACCCCGGGCCGCAAGGTGTGTCTCGGCACTC 482  
QY 150 GCTGCCCCTTCTGAGTCCCTGGACATCAAGACGAGCAAGATGAAGCAGGTCAAGTTTCA 209  
Db 481 TGGGGCTTCGCCAAGTACGTGGCCGGCTGGAGCTGGTGTGAAGATGCCCGAGGTGCT 422  
QY 210 GAGCTTCTGTGTTTGGGGAGCAGACCAATACAAGGGCCGGAAGCATGTACGACGCAACGC 269  
Db 421 CGGCACCGGTGAGGGCGGCGAAATCATCAGCCAGGACTACCGCGTGTTCGCCATGACGC 362  
QY 270 CCATCTGCTCAAGGGCAGCGCTGGACCAACCGCACTTTGACAAGATCAAGCAGTACCT 329  
Db 361 CCTGTGTGGACGACGCCATGCGCGCTTCCGCCACGACACACAGCGGTGTCTTGGGAGGA 302  
QY 330 TGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGG 364  
Db 301 GGGCCAGTTCTCGGACGAGCGAGTCCGTGAGG 267

## RESULT 8

US-09-902-540-5853  
; Sequence 5853, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5853  
; LENGTH: 603  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(603)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-5853

Query Match 7.3%; Score 43.4; DB 3; Length 603;  
Best Local Similarity 45.4%; Pred. No. 0.097;  
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;  
QY 30 CACAGAGACGCGGAGCGGATCGGGCGGCAAGACTGTTTGTATGACCTGGGCGGCGC 89  
Db 3 CGCAATCCCGGNCGTGTGGCGGTGGACNCGGTGATGGTGGCCACCTGCACGTGCT 62  
QY 90 AGAAGGCATGAAGCTGGCGGTGTGACACCTTCTACGATAAGTGTGCTGACCCGGAGCT 149  
Db 63 GCTCAACCGCGCAGCTGTCTACCGACCCCGCGCGCAAGTGTGTGTCGGCACTC 122  
QY 150 GCTGCCCTTCTGAGTCCCTGGACATGCAAGACAGACAGATGAAGCAGGTCAAGTTTCA 209  
Db 123 TGGCGCCTTCTGCCAAGTACGTGGGCGCGCTGGAGCTGTGTGTAAGATGCCCGAGGTGCT 182  
QY 210 GAGCTTCTGTGTTTGGCGGAGCAGACCAATACAAGGGCCGGAAGCATGTACGACGCAACGC 269  
Db 183 CGGCACCGGTGAGGGCGGCGAATATCATCAGCCAGACTACCGCGTGTTCGCCATGGAGCG 242  
QY 270 CCATCTGCTCAAGGGCCACCGCTTGGACCAACCGCACTTTGACAAGATCAAGCAGTACCT 329  
Db 243 CCTGTGTGCGACGCGCATGCGCGCTTCCGCCACGACACACGCGTGTCTCGGAGGA 302  
QY 330 TGGAGAGACGCTGCAAGAGATGGCGGTCAAGCAGG 364  
Db 303 GGGCCAGTTCTCGGCGACGAGCGAGTCCGTGAGG 337

## RESULT 9

US-09-902-540-3555  
; Sequence 3555, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 3555  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-3555

Query Match 7.2%; Score 42.8; DB 3; Length 585;  
Best Local Similarity 48.4%; Pred. No. 0.14;  
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;  
QY 78 CCTGGGCGCGCAGAGGCGATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGCTGGC 137  
Db 18 CGTGGCGATCGCGGGCTGCTCCACCTGGGAGCGGTCTTCTTCGAGCGGATGCCAG 77  
QY 138 TGACCCGGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGACAGAGATGAAGCA 197  
Db 78 CCAGGCGCAGATGCTGCGGAGCATCGAAGCTGGACAGAGAGAGGCGCCAGCAGACCA 137  
QY 198 GGTCAAGTTTCAAGCTTCTGTTTGGCGGAGCAGACCAATACAAGGGCCGGAAGCATGTA 257  
Db 138 GGCTCATCATCAGCAAGTGGGAGAGCGCGCGGGGACCCCGGAGGACAGCTACGATTG 197  
QY 258 CGAGCGCACACGCCCATCTGTCAAGGGCCAGCGCTGGACCCGACCCGACCTTTTGACAAGAT 317  
Db 198 CTCCTGCGGAGCAGTGTGGTGGCTGCGACGACCCCACTCCCGCGTCGAGAGAGCT 257  
QY 318 CAAGCA 323  
Db 258 CAAGCA 263

## RESULT 10

US-09-902-540-1171  
; Sequence 1171, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1171  
; LENGTH: 19019  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(19019)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1171

Query Match 7.2%; Score 42.8; DB 3; Length 19019;  
Best Local Similarity 48.4%; Pred. No. 0.39;  
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 78 CTTGGCGCGGAGAGGATGAAGCTGGCGTTGACACCTTCTACGATAAGTGTCTGGC 137  
DB 9777 CGTGCCCATCGCGGGGCTGCTCACTGGAGACGGCTCTTCTTCGAGCGGATGCCAG 9836

QY 138 TGACCCGGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGAGCAGAAGATGAAGCA 197  
DB 9837 CCAGGCGCAGATGCTGGCGAGCATCAGAAGCTGGACAAGAGGAGGCCCGCAGACCAA 9896

QY 198 GGTCAAGTTCATGAGCTTGTGTTTGGCGAGCAGACCAATACAAGGCGCGAAGCATGTA 257  
DB 9897 GGCCTGCATCAGCAAGTGGCGAAGCGCGCGGGGACCCCGCGAGCAGACTTACGATTG 9956

QY 258 CGAGGCACACGCCCATCTGTTCAAGGGCCACGCGCTGGACCCAGCTTTGACAAGAT 317  
DB 9957 CTCCTGCGGAGCAGTGTGATGGCTGGCAGCAGACCCCAACCTCCCGCTCGGAGAAGCT 10016

QY 318 CAAGCA 323  
DB 10017 CAAGCA 10022

RESULT 11  
US-09-744-072-1  
; Sequence 1, Application US/09744072  
; Patent No. 6825328  
; GENERAL INFORMATION:  
; APPLICANT: SCHERER, STEPHEN W.  
; APPLICANT: MINASSIAN, BERGE A.  
; APPLICANT: ROULEAU, GUY  
; APPLICANT: DALGADO-ESCUETA, ANTONIO  
; TITLE OF INVENTION: LAFORA'S DISEASE GENE  
; FILE REFERENCE: 086671/0113  
; CURRENT APPLICATION NUMBER: US/09/744,072  
; CURRENT FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: 60/093,495  
; PRIOR FILING DATE: 1998-07-20  
; PRIOR APPLICATION NUMBER: 60/130,269  
; PRIOR FILING DATE: 1999-04-21  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3128  
; TYPE: DNA  
; ORGANISM: Homo sapiens

Query Match 7.1%; Score 42.6; DB 3; Length 3128;  
Best Local Similarity 50.7%; Pred. No. 0.26;  
Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 GCCTGCTGCTGACAGCGGCGCCACAGCACCACAGAGACGCGGAAGCGGATCGGGCGC 60  
DB 22 GTGTGTCACCCCGCTGGCGCGCGCGCGCGAGCTGCTGTGGTGGGTGCGGGCC 81

QY 61 AGAAGCTGTTTATACCTGGCGCGCGCGAGAGGATGAGCTGGGGTTGACCTTC 120  
DB 82 GAGCTGGGGGCTTGGAGCGCGCGGTGCGCTCGCTGAGGCGCGCGCACCGCGCG 141

QY 121 TAGATAAGTGTGCTGACCGCGAGCTGCTCCCTTCTTCAGTCCCTGGACATGCAA 180  
DB 142 GCGAGCGGGCCCTTGGCGCTGCGAGGACCGGGCTGTGGCTGGGAGGTGGAGCTGGCG 201

QY 181 GAGCAGAAGATGAAGCAGGTTC 201  
DB 202 GCCGAGGAGCGCGCGCAGGAC 222

RESULT 12

US-09-949-016-16800

; Sequence 16800, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16800  
; LENGTH: 26896  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-16800

Query Match 7.1%; Score 42.4; DB 3; Length 26896;  
Best Local Similarity 47.7%; Pred. No. 0.55;  
Matches 124; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 137 CTGACCCGGAGCTGCTGCCCTTCTTCGAGTCTCGACATGCAAGAGCAGAGATGAAGC 196  
DB 22334 CAGACCATGTGCCACTCTCTCTGACACAGCGGCCCATGATGGCAGAGGAGTGAAGA 22393

QY 197 AGGTCAAGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCCGGAAGCATGT 256  
DB 22394 AGGAGCAGCAGACACCGCCACTCTGGAGCGCATGAAGAAGAACATGAAGACAGACCATTA 22453

QY 257 ACAGCAGCAGACCGCCATCTGTTCAAGGGCCAGCGCTGACACCAACCCCACTTTGACAAGA 316  
DB 22454 AGGACCTGCGAGCAGCGCGCTGGAGCGAAGCGCAGACATCGCCCTCAAGGGCGGCAAGAAGC 22513

QY 317 TCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGAGATGTGATCCAGC 376  
DB 22514 AGCTGAGAGCTGGAAGCGCGGTGCGGAGCTGGAGATGAGTGGAGGCGGAGCAGA 22573

QY 377 ACGCCCGCGGAGTGGTGAG 396  
DB 22574 AGCGCAAGCAGAGTCGGTG 22593

RESULT 13

US-09-252-991A-11092  
; Sequence 11092, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 11092  
; LENGTH: 759  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-11092

Query Match 7.1%; Score 42.2; DB 3; Length 759;  
Best Local Similarity 51.9%; Pred. No. 0.21;



Result No.	Score	Query Match	Length	DB	ID	Description
1	254.5	22.7	124	4	US-10-282-122A-61519	Sequence 61
2	148	13.2	324	4	US-10-425-114-58160	Sequence 58
3	142.5	12.7	19723	4	US-10-084-846A-5	Sequence 5
4	125	11.1	417	4	US-10-437-963-143835	Sequence 14
5	125	11.1	19695	4	US-10-084-846A-3	Sequence 3
6	124.5	11.1	19662	4	US-10-084-846A-6	Sequence 6
7	120.5	10.7	19608	4	US-10-084-846A-8	Sequence 8
8	119.5	10.7	276	4	US-10-437-963-166380	Sequence 16
9	117.5	10.5	384	4	US-10-425-114-72136	Sequence 72
10	117.5	10.5	384	4	US-10-425-114-72137	Sequence 72
11	117.5	10.5	19723	4	US-10-084-846A-5	Sequence 5

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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61519
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Legionella pneumophila
US-10-282-122A-61519

Alignment Scores:
Pred. No.: 9,08e-16 Length: 124
Score: 254.50 Matches: 49
Percent Similarity: 64.1% Conservatives: 26
Best Local Similarity: 41.9% Mismatches: 41
Query Match: 22.7% Indels: 1
DB: 4 Gaps: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)
QY 61 AAGAAGCTGTTGATGACCTGGCGGCGGAGGAGGATGAGCTGGCGGTTGACACCTTC 120
Db 3 GluSerLeuPheGluArgLeuGlyGlnAsnAlaValAsnThrAlaValAspIlePhe 22
QY 121 TACGATAAGTGTGGCTGACCCGAGCTGCTGCCCTTTCGAGTCCCTGGACATGCAA 180
Db 23 TyrArgLysMetLeuMetAspArgValAsnTyrPhePheAspValAspMetGlu 42
QY 181 GACGAGAAGTGAAGGCTCAAGTTCATGAGCTTGTGTTGGCGGAGCAGACCAATAC 240
Db 43 GlnGlnIleLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
QY 241 AAGGGCGAAGCATGTACGACGACGACGCGCCATCTGGTCAAGGCGCACCGCTGGAC 300
Db 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
QY 301 CGCCACTTTGCAAGATCAAGCAGTACTCTTGGAGAGACGCTGCAAGAGATGGCGTCAAG 360
Db 82 SerHisValAspIleValIleGluHisLeuGlyGlnThrLeuLysGluLeuGlyAlaAsn 101
QY 361 CAGAGTGTATCCAGCAGCGCGCGGAGTGGTGGATGCCACCGCGCAGAA 411
Db 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2
US-10-425-114-58160
; Sequence 58160, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58160
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI.pep
US-10-425-114-58160
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Alignment Scores:
Pred. No.: 2,66e-05 Length: 324
Score: 148.00 Matches: 62
Percent Similarity: 28.1% Conservatives: 18
Best Local Similarity: 39.1% Mismatches: 77
Query Match: 13.2% Indels: 53
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)
QY 5 TGCCTGCAGACGCGG-----CCACGACGACGACGAGAGCGGCGGAGACGG 49
Db 84 CysAlaAlaArgThrArgAlaAlaArgThrThrAlaProSerAlaProCysThrArgArgThr 103
QY 50 GATCGCGGCGCAGAGAGCTGTTGTATGACCTGGCGCGCAGAGGACGATCAAGCTGGCGG 109
Db 104 SerSerGlySerArgAlaCys-----CTGACCGGAGAGCTGCTGC 110
QY 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTGACCGGAGAGCTGCTGC 154
Db 111 -----ProSerAlaAlaThrCysTyrArgTyrAlaAlaThrArgSerArgProThrSer 128
QY 155 CTTCTTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGAGGTCAAGTTCATGAGCT 214
Db 129 ProArgTyrGlyProThrCysCysProSerProSer-----SerCysSerSerSerArgAla 147
QY 215 TCGTGTTCGCGGAGCAGACCAATACAGGCGGAGCATGTACGACGACGACGACGCGCCATC 274
Db 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGln 167
QY 275 TGGT-----CAAGGCGCACGCGCTCGACGACGCGCCACTTTGACAAAGATCAAGCAGTACC 328
Db 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerSerThr 186
QY 329 TTGGAGAGACGCTGCAAGAGA-----TGGCGCTCAAGCAGGAGTGTGATCC 373
Db 187 -----SerAlaCysThrArgProAlaAlaThrCysTyrSerThrCysArgAlaThrTyr 204
QY 374 AGCAGCGCGCGGAGTGGAGTCCACCGCGGACGCAATTTGACTTNCACCAACTGCG 433
Db 205 AlaCysAlaThrProThrTyrArgProProAlaProArgCysThrAlaSerAlaThr--- 223
QY 434 CACCCAACTGATTTTCAATTAACCAACCCAGCGCTGACGCGCTCATTCATCGATTTTGAG 493
Db 224 -----ProGlnAlaAlaSerGlyThrSerTyrArg 234
QY 494 -----CGGGAGCGCCAGTTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCA 541
Db 235 ThrTyrArgProArgAlaAlaSerAlaAlaAlaThrAlaSerGlySer---SerProSer 253

RESULT 3
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
```



; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 5

; LENGTH: 19723

; TYPE: PRT

; ORGANISM: Streptomyces viridochromogenes

; FEATURE:

; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.

; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.

US-10-084-846A-5

Alignment Scores:

Pred. No.:	0.000264	Length:	19723
Score:	142.50	Matches:	63
Percent Similarity:	35.0%	Conservative:	16
Best Local Similarity:	27.9%	Mismatches:	68
Query Match:	12.7%	Indels:	79
DB:	4	Gaps:	12

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY	5	TGCTGCAGACGGCCACAGCACCACAGACGGCGGATCGGGCGCAAGA	64
DB	4635	CysAlaAlaArgSerProSerPro	-----AlaTrpSerThr 4647
QY	65	AGCTGTTTATGACCTGG	-----GGGGCGCAGAGGCATGAGCTGGCGGTG 112
DB	4648	SerAlaProAlaThrTrpSerTrpThrSerAlaAlaThrAlaProCysTrpArgPro	4667
QY	113	ACACCTTCTACGATAAGTGTGGCTG	-----139
DB	4668	ThrProProThrGlyProAlaThrSerGluTrpThrProProProSerSerProArg	4687
QY	140	-----ACCCGG-----AGCTGCTGCCCTTCTCGAGTCCCTGGACATGCAAGACGAGAAGA	190
DB	4688	ProThrArgArgAlaSerSerProThrSerSerHisThrCysSerAlaGlyAla	4707
QY	191	TGAAGCAGTCAAGTTCATGAGTTCGTGT	-----TTGGCGGAGCGAGCC 235
DB	4708	AlaProArgSerSerProArgSerArgCysSerThrThrCysArgValProTrpSerSer	4727
QY	236	AATACAAAGGGCGAAGCATGTACGAG	-----262
DB	4728	CysGlyArgSerAlaAlaCysArgThrThrAlaSerGlyProSerArgAlaIleCysPro	4747
QY	263	-----CACACGCC-----AFTCGTCAAGGGCCACCGCTCGACACCGCCACT	307
DB	4748	ArgCysSerThrProAlaProThrThrTrpSerAlaThrSerThrTrpThrThrGly	4767
QY	308	TTGACAAAGTCAAGCAGTACCTTGGAGACCGCTGCAAGAGATGGCGCTCAAGCAGGATG	367
DB	4768	CysAlaArgSerSergly	-----TrpProSerAla-----4777
QY	368	TGATCCAGACCGCCGGAGTGTGG	-----AGTCACCGCGAGCAATTTGACTTNC 421
DB	4778	-----ProAlaArgTrpTrpMetProSerProSerProSerThr--AlaGluAlas	4793
QY	422	CCAACAACCTGCGCACCACCACTGATTTTCATTAACCCAA	-----459
DB	4793	erArgSerCysTrpProAlaAlaAlaProLeuAlaArgSerThrSerArgArgTrpProA	4813
QY	460	-----CCCCAGCTGAGCGCTCATTCATCGATTTTGGAGCGGGAGCGCCAGTTCGCCAGCGC	517
DB	4813	laSerAlaProGluArgArg	-----ThrCysProThrArgSerS 4826
QY	518	GCCAGGGGGCCCA	531
DB	4826	erProGlyGlyPro	4830

RESULT 4

US-10-437-963-143835

; Sequence 143835, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 143835  
; LENGTH: 417  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_44705C.1.pap  
US-10-437-963-143835

Alignment Scores:	0.0049	Length:	417
Pred. No.:	125.00	Matches:	63
Score:	36.2%	Conservative:	13
Best Local Similarity:	30.0%	Mismatches:	74
Query Match:	11.1%	Indels:	60
DB:	4	Gaps:	10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

QY	23	CCAGCACCACAGAGACGGCGAAGCGGATCGGGCGCAAGAAGCTGTTGTGACCTGG	82
DB	22	ProThrProHisArgArgGlu	-----ileGluArgTrp 32
QY	83	GGGGCGCAGAGGATGAGCTGGCGGTGACACCTTCTACGATAGGTGGTGGTACC	142
DB	33	Leu	-----ProTrpArgSerAlaProProPro-----ThrThr 43
QY	143	CGAGCTGTGC	-----CCTTCTCGAGTCCCTGGACATGCAAGAGCAGA 187
DB	44	GlySerCysSerThrProThrThrProProThrProProProThrThrThrSer	62
QY	188	AGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCC	247
DB	63	-----SerArgSerLeuProProAlaThrProProProAlaProThrIlysArg	79
QY	248	GAAGCATGTACACGCCACACGCCCATCTGGTCAAGGCCACCGCTGGACACCGCCACT	307
DB	80	-----ArgThrThrArgTrp-----GlyAlaThr 87	
QY	308	TTGCAAGATCAAGCAGTACCTTGGAG	-----AGACGCTGCAAG 346
DB	88	LeuThrAlaThrThrSerThrAlaGluAsnSerArgArgArgArgAlaArgArg	107
QY	347	AGATGGCGCTCAAGCAGATGTGATCCAGACCGCGCGGAGTGGTGGAGTCCA	400
DB	108	ArgArgGlyArgSerArgAlaSerSerThrThrProProProThrThrSerProGlyThr	127
QY	401	-----CCCCGCGAGAAATTTGACTTNCACAACTCGCGACCCCAACTGATTTTCATTAACCC	457
DB	128	SerProSerThrProSerAlaProSerThrSerSerProThrArgAlaSerProPro	147
QY	458	AACCCAGCTGAGCGCTCATTCATCGATTTTGGCGGGGAGCGCCAGTTCGCCAGCGC	517
DB	148	TyrArgSerThrSerProSerSerProPro--ProAlaAlaSerSerAlaSerAlaAla	167
QY	518	GCCAGGGGGCCCA	-----GGAGCTGCAATCGTTTG 550
DB	167	rgProProAlaProThrThrSerProThrArgProProSerGlyCysAlaSerLeu	187
QY	551	CCAGCCCTTGTCTGCTTGAAGGCCA	576



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QY 233 TCTGCTCCGCCAAACAG-----216
|||:|||||:|:|
19429 SerSerProSerProArgProGlyCysThrGluGlyArgSerProValSer 19448
|||:|||||:|:|
QY 215 -----AAGCTCATGAACCTTGACCTGCTTCATCTCTGCTCTTGCATGTCAGG 168
|||:|||||:|:|
19449 SerProHisGlyArg-SerGlyCysTrpProAlaGlyProArgProAlaAlaGlyProG 19468
|||:|||||:|:|
QY 167 GACTCGAAGAGGCGAGCAGCTCCGGGTGAGCCAGCAGCAGCTTATCGTAGAAGGTGTCAACC 108
|||:|||||:|:|
19468 YAspArgArgGlnAlaLeuSerSerGlySerPro-----19479
|||:|||||:|:|
QY 107 GCAGCTTCATGCTTCTGCGCGCCAGCTCATCAAGCAGCTTCTTGGCGCCGCGATCCC 48
|||:|||||:|:|
19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgIleAl 19493
|||:|||||:|:|
QY 47 GCTTCG-----CGTCTCTGCTGGTGGTGG 20
|||:|||||:|:|
19493 alaProThrIleProAlaLeuPheCysSerTrp 19504
|||:|||||:|:|
RESULT 7
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8
Alignment Scores:
Pred. No.: 0.0363 Length: 19608
Score: 120.50 Matches: 49
Percent Similarity: 35.7% Conservative: 16
Best Local Similarity: 26.9% Mismatches: 92
Query Match: 10.7% Indels: 25
DB: 4 Gaps: 7
US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)
QY 20 CCACGACGACACAGAGCGGCGGAGCGGATCGGGCGCGCAAGAGCTGTTGTATGACC 79
|||||:|:|
5430 ProProAla-----SerSerThrArgCysCys-----5438
|||||:|:|
QY 80 TGGCGCGCGCAGAGGATGAAGCTGGCGGTGACACCTTCTACGATAGGTTGGCTG 139
|||||:|:|
5439 -----ProProAlaSerThrTrpArg-----SerThrAlaAlaCysTrpPro 5452
|||||:|:|
QY 140 ACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGACGACAGAGATCAAGCAGG 199
|||||:|:|
5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgProGlyArg 5470
|||||:|:|
QY 200 TCAGTTTCATGAGCTTCGTGTTTG---GCGGAGCAGACCAATACAGGCCGGAAGCATGT 256
|||||:|:|
```

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Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTrpCysProAlaCys 5490
QY 257 ACAGCGCACACGCCCTCTGGTCAAGGGCCACGCGCTGGACACCGCCACTTTGACAAGA 316
|||||:|:|
5491 ThrSerAsnArgProAlaArgProProThrSerTrpProThrArgProArgSerAla 5510
|||||:|:|
QY 317 TCAGCAGTACCTTGGAGAGAGCTGCAAGATGGCGTCAAGCAGGATGTATCCAGC 376
|||||:|:|
5511 ProArgProSerThrSerArgSerThrAlaArgTrpProSerProAsnTrpSerArgAsp 5530
|||||:|:|
QY 377 ACGCCCGCGAGTGGTGGAGTCCACCGCGAGCAATTTGACTTNCACAACA-----ACT 430
|||||:|:|
5531 TrpProThrSerThrProSerProAlaArgThrArgThrAlaProSerArgArgThr 5550
|||||:|:|
QY 431 GCGCACCCCACTGATTTTTCATTAAACCAACCCAGCAGCTGAGCGCTCATTCATCGATTTT 490
|||||:|:|
5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg-----5567
|||||:|:|
QY 491 GAGCGGGAGCGCCAGTTGCCGAGGCGGCCAGGGGGCCAGGAGCTGCAATCGTTTG 550
|||||:|:|
5568 ArgProArgThrProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeu 5587
|||||:|:|
QY 551 CCAGCC 556
|||||:|:|
Db 5588 ProAla 5589
|||||:|:|
RESULT 8
US-10-437-963-166380
; Sequence 166380, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 166380
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(276)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_65095C.1.pep
US-10-437-963-166380
Alignment Scores:
Pred. No.: 0.0151 Length: 276
Score: 119.50 Matches: 52
Percent Similarity: 35.1% Conservative: 15
Best Local Similarity: 27.2% Mismatches: 69
Query Match: 10.7% Indels: 55
DB: 4 Gaps: 8
US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)
QY 29 CCACAGACGCGCGGAGCGGATCGGGCGCGCAAGAGCTGTTGTATGACCTGGCGGCG 88
|||||:|:|
3 ProArgArgArgArgArgArgIleCysThrValArg-----14
|||||:|:|
QY 89 CAGAAGGATGAAGCTGGCGGTGACACCTTCTACGATAGTGTGCTGACCGGAGC 148
|||||:|:|
```

```
Db 15 -----ArgProThrAlaThrThrThr-----ThrThrThrSer 25
QY 149 TGCTGCCCTTCTTCGAGTCCTCGACATGCAGAGCAGAGATGAAGCAGGTCAAGTTCA 208
Db 26 AlaSerProSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTGGCGGAGCAGACCAATACAAAGGCGCGAAGCATGTAGCAGC----- 262
Db 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACAGCCCATCTGCTCAAGGGCCACCGCTCGACCCACCCACTTTGACAAAGATCA 319
Db 60 ProSerSerProSerHisGlySerArgSerProTrpThrGlyThrThrSerSerProSer 79
QY 320 AGCAGTACCTTGGAGAGACCTGC-----AAGAGATGGCGCTCAACGACGATGTGA 370
Db 80 ArgSerGlySerCysArgGlyCysCysPheArgArgArgTrpArgSerThrArg----- 97
QY 371 TCAGCAGCGCGCGGAGTGTGTGAGTCCACCGCGCAGCAATTTGACTTNNCCCAACAAC 430
Db 98 -----ProProAlaProSerSerAlaSerProThrGly 108
QY 431 GCGCACCACCACTGATTTTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTT 490
Db 109 AlaSerThrThrSer-----ProSerProThr----- 117
QY 491 GAGCGGGAGCGCGCAGTTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 550
Db 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAlaSerGlySer***Cys 133
QY 551 CCAGCCCTTGTGCTGCAATTGAAGGCCATCAGCCCA 583
Db 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

RESULT 9
US-10-425-114-72136
; Sequence 72136, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72136
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI.pep
US-10-425-114-72136

Alignment Scores: 0.0257 Length: 384
Pred. No.: 117.50 Matches: 69
Percent Similarity: 37.9%
Best Local Similarity: 30.8% Mismatches: 74
Query Match: 10.5% Indels: 65
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

QY 15 CGCGGCCACAGCNC-----CACAGAGCGCGGAGCGGATGCGGGCGCAAGAGCT 68
Db 54 ArgGlyHisArgHisSerSerHisArgProLeuAlaSerGlyArgGln----- 69
```

```
QY 69 GTTTGATGACCTGGGCGCGCAGAGGCATGAAGCTGGC----- 107
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACTTCTACGA-----TAAGGTGCT 134
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgArgArgGlyAla 104
QY 135 GCGTACCGCGGAGCTGCTCCCTTCTTCAGTCCCTCGACATGCA-----AGAGCA 185
Db 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgGlyAla 124
QY 186 GAAGTAGAAGCAGGTCAAGTTGATGAGCTTCGTGTTGGCGGAGCAGCAATACAAAGGG 245
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGlyGly 144
QY 246 -----CCGAAGCATGTACAGCGCACACGCCCATCTGCTCAAGGGCCA 287
Db 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACCAACCGCCACTTTGACAAAGATCAA 320
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGT-----CAAGCAGGATGT 368
Db 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGGAGCAAT---TTGACTTNCCTCAA 425
Db 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221
QY 426 CAACTCGCGCACCAACTGTTTTCATTAAACCCCAACCCAGCCCTGAGCGCTCATTCATCG 485
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234
QY 486 ATTTTGAGCGGGAGCGCCAGTTCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
Db 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGCCA 553
Db 253 roValPro 255

RESULT 10
US-10-425-114-72137
; Sequence 72137, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72137
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3061-057-C6_FLI.pep
US-10-425-114-72137

Alignment Scores: 0.0257 Length: 384
Pred. No.: 117.50 Matches: 69
Percent Similarity: 37.9%
Conservative: 16
```

```
Best Local Similarity: 30.8% Mismatches: 74
Query Match: 10.5% Indels: 65
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72137 (1-384)
QY 15 CCGCGCCACACAC-----CACAGACGCGGAGCGGATCGCGCGCAAGAGCT 68
DB 54 ArgGlyHisArgHisSerHisArgProLeuAlaSerGlyArgGln-----69
QY 69 GTTGTGATCGTGGCGCGGACAGGCGCATGAAGCTGGC-----107
DB 70 -----ArgArgArgGlyArgAlaGlyArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGGTGCT 134
DB 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgArgAlaArgArgGlyAla 104
QY 135 GGCTGACCGGAGCTGCTGCTCCCTTCTGAGTCCCTGGACATGCA-----AGAGCA 185
DB 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGluGlyArgAla 124
QY 186 GAAGATGAAGCAGGCTCAAGTTCATGAGCTTCCTGTTGGCGGAGCAGACCAATCAAGG 245
DB 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTATACACGACGACACGCGCCATCTGTCACAGGGCCA 287
DB 145 LeuGluGlyGlyValArgProArgAlaAlaAlaAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CTGACACACCGCCACTTTGACAGATCAA 320
DB 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGAGAGACGCTCAAGAGATGGCGT-----CAAGCAGATGT 368
DB 184 AlaGlyGlyValArgGlySer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGACGCGCGGAGTGGTGGAGTCCACCGCGACGAAT---TTGACTTCCCAA 425
DB 202 Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuGlnGlyProA 221
QY 426 CAACTGCGCACCACTGATTTTCAATTAACCAACCCGCTGAGCGCTCATTCATCG 485
DB 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu-----234
QY 486 ATTTGAGCGGAGCGGAGTGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 545
DB 235 -----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTGGCCA 553
DB 253 rovalpro 255

RESULT 11
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREPZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 5
; LENGTH: 19723
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 0.0712 Length: 19723
Score: 117.50 Matches: 64
Percent Similarity: 32.9% Conservative: 13
Best Local Similarity: 27.4% Mismatches: 86
Query Match: 10.5% Indels: 71
DB: 4 Gaps: 15

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)
QY 556 GGCTGGCAACGATTTGAGGCTCTGGGCGCCCTGGGCGGCTCGGC-----509
DB 16445 GlyAlaGlnArgArgCysHisArgThrGlyProIleGlyLysSerGlyAlaGlyProGly 16464
QY 508 -----AACTGGCGCTCCCGCTCAAAATCGATGGAATG 476
DB 16465 ThrAlaAlaArgGlnArgLeuValArgSerArgTrpProMetSerAlaSerAlaPhe 16484
QY 475 AGCGCTCAGGCTGGGGTTTGAATGAAATCACTGGGTGCGCAGTTGT-----425
DB 16485 SerTrpLeuValGlyArgGly-----SerTrpAlaValSerCysAlaArgThr 16500
QY 424 -----TGG-----GNAAGTCAAAATCTGT 407
DB 16501 ProArgProGluProArgTrpArgArgSerProGlyGlyTyrArgThrSerProCysArg 16520
QY 406 CCGCGG-----TGACTCCACCACTCCGCGCGGCTGGTGGATCATCATCTGCTTCA 356
DB 16521 AlaGlySerSerSerTrpThrSerPro---ProArgArgProGlyAsnTrpProThrSer 16539
QY 355 CGCCCATCTCTTGCAGCGCTCTCCCAAGGTACTGCTGTATCTTGTCAAAGTGGCGGTGT 296
DB 16540 ThrProSer-----AlaArgThrArgTrpSerThrProSerAlaAlaThrGlyGlySer 16557
QY 295 CCAGCGCGTGGCGCTTGACCAAGATGGCGTGTGCGT---CGTACATGCTTCGCGCCCTGT 239
DB 16558 ProAsnGlyThrTrpArgProThrAlaArgCysArgProAlaAlaCysTrpThrArgCys 16577
QY 238 ATTGCTCTGCTCCGCAACAGCAAGCTCATGAACCTGACCTGCTCATCTCTGCTCTT 179
DB 16578 GlyGly-----ProArgAlaVal-----ProThrSerSerThrSerAla 16590
QY 178 GCATGT-----CCAGGAGCTCGAAGAAGG---155
DB 16591 GlnCysTrpSerThrAlaArgProArgProValAsnArgProGlyProArgArgArgPro 16610
QY 154 GCAGCAGCTCCGCGGTGACCCAGCACCTTATCTAGAGGTGTCAACCGCAGCTCATGC 95
DB 16611 GlyArgArgProProThrAlaArgProAsnSerArgArgAlaArgPro-----Cys 16627
QY 94 CTTCTG-----CGCGCGCCAGGTCAATCAACAGCTTCTTTCG-----59
DB 16628 TrpArgProProArgArgAlaSerTrpArgArgAlaCysCysGlySerProThrTrpPro 16647
QY 58 GCCCGCATCCCGCTCCCGCGCTCTCTGTGGTGTGCTGGTGGCGG 17
DB 16648 GlyArgAlaProArgArgSerAlaCysSerAlaGlyTrpPro 16661

RESULT 12
US-10-084-846A-7
; Sequence 7, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
```

:	APPLICANT:	MUHLNWEG, AGNES			
:	APPLICANT:	TREFFER, AXEL			
:	APPLICANT:	BECHTHOLD, ANDREAS			
:	TITLE OF INVENTION:	AVILAMYCIN DERIVATIVES			
:	FILE REFERENCE:	1974-005			
:	CURRENT APPLICATION NUMBER:	US/10/084,846A			
:	CURRENT FILING DATE:	2003-02-25			
:	PRIOR APPLICATION NUMBER:	PCT/EP01/09815			
:	PRIOR FILING DATE:	2001-08-24			
:	PRIOR APPLICATION NUMBER:	DE 101 09 166.4			
:	PRIOR FILING DATE:	2001-02-25			
:	NUMBER OF SEQ ID NOS:	120			
:	SOFTWARE:	PatentIn Ver. 3.2			
:	SEQ ID NO 7				
:	LENGTH:	19652			
:	TYPE:	PRT			
:	ORGANISM:	Streptomyces viridochromogenes			
:	FEATURE:				
:	OTHER INFORMATION:	Protein 2: amino acid sequence encoded by coding strand 2.			
:	OTHER INFORMATION:	Start codon: gat, Start position: nucleotide 2.			
US-10-084-846A-7					
Alignment Scores:					
Pred. No.:            0.089            Length:            19652					
Score:               116.50          Matches:            73					
Percent Similarity: 33.0%          Conservative:        14					
Best Local Similarity: 27.7%       Mismatches:         93					
Query Match:        10.4%       Indels:              84					
DB:                                   Gaps:                13					
US-0 <sub>g</sub> -920-953-2 (1-598) x US-10-084-846A-7 (1-19652)					
Qy	598	GGCTTGGTCGAAATGGGTAGTGCTCTCAATGCACG-----AAG 557			
Db	6432	GlyTTProThrArgTrpThrArgProProGlyCySProSerProSerProArgValArg 6451			
Qy	556	GGCTGCGCAAACGATTTCGAGGCTCCTGGGCCCCCTGGCGCGCTCGGCAACTGGCGTCC 497			
Db	6452	ProTIPCySthProCys-----AlaLeuAgIlleThrArgAla 6464			
Qy	496	CGCTCAAAATCGATGGAAATGAGCGCTCAGGCTGGGTTGGGTTAATAAATCAGTTGG 437			
Db	6465	ProIle-----SerProThrArgArgAlaGlyProMet-----6475			
Qy	436	GTGCGCAGTTGTTGGNNAAGTCAAATTGCT-----407			
Db	6476	-----CysTrpSerSerTrpGlyArgProLysArgSerProThrProSerArgAla 6492			
Qy	406	CGCGGTGGACT-----CCACCACCTCCGCGCGCTGCTGGATCA 368			
Db	6493	ProGlyTIPThrArgThrAspValProArgProGlyArgSerThrArgSerGlyPro 6512			
Qy	367	CATCTCGTTGACGCCCATCTCTTGAGGGTCTCTCAAGGTACTGCTTGATCTTGT---311			
Db	6513	ArgProLeuThrSerArgSerLeuArgProAlaAlaCysGlyThrAlaProHisThrVal 6532			
Qy	310	---CAAAGTGGCGGTGGTCCAGCGCTGSCCCTTCACCATGCGGTGTCGTCGTACA 254			
Db	6533	ArgArgSerSerHisGlyProThrThrGlyProProHisAlaGlyProArgArgMetPro 6552			
Qy	253	TGCTTCGGCCCTTGATTGCTGTCTGCTCGCCAAAACAGAAGCTCATGAACCTTGACCT---197			
Db	6553	AlaAlaLeuProGlySerGlyValLeuArgArgAlaArgSerArgCysArgGlleProArg 6572			
Qy	196	-----GCTTCATCTTCTGCTCTTGCAATGTCCAGGACCTCGAAGA---158			
Db	6573	LeuArgArgProArgAlaArgSerArgProGlySerArgCysPrcCysProArgArgGlu 6592			
Qy	157	---AGGCAGCAGCTCCGGGTGAGCCNGCA-----CCTTATCTAGTAAGGTGTCAACCG 107			
Db	6593	CysArgSerArgArgProArgArgProSerHisProAlaArgThrArgCysArgPro 6612			
Qy	106	CCAGCT-----TCATGC 95			

```

Db      6613 ThrAlaArgProProGlyThrTrpProAlaProArgValArgArgAlaGlyArgAla 6632
QY      94 CTTCTGGCGCCGCCAGGTCTCAACACAGT----- 65
Db      6633 AlaAlaArgArgProProHisArgSerAlaArgArgSerSerArgThrGlyGluSerArg 6652
QY      64 ---TCATTGGCGCCGCATCCCGCTTCGCCGCTCTCTGT---GGTGCTGGTGGCGCGCTCTG 11
Db      6653 ArgSer-ThrProAlaProArgArgAlaArgProAlaProGlyAlaGlyArgArgAl 6672
QY      10 CAGCAGCGC 1
Db      6672 aArgThrArg 6675

RESULT 13
US-10-437-963-103601
; Sequence 103601, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103601
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101013C.1.pep
US-10-437-963-103601

Alignment Scores:
Pred. No.:          0.0318       Length:         155
Score:             115.50        Matches:         48
Percent Similarity: 36.9%        Conservative:    7
Best Local Similarity: 32.2%     Mismatches:     49
Query Match:       10.3%         Indels:         45
DB:                4            Gaps:           9

US-09-920-953-2 (1-598) x US-10-437-963-103601 (1-155)
QY      385 CGGCGGGTGTGTGATCATCATCTCTTGACGCCCATCTCTTGACCGCTCTCTCCAAGGT 326
Db      19 ArgargAlaProThrHisGluPro-----ProSerSerProargAlaGlyArgSer 36
QY      325 ACTGCTTGATCTCTGCAAGTGGCGGT-----GGTCAGGCCGTGGC 284
Db      37 ArgSerArgSerCysThrsSerAlaProargArgCysHisArgIleAlaProGlyArgGly 56
QY      283 -----CCTTGACCAGATGGCGTGGCTGCTGCTACATGC 251
Db      57 ArgCysArgArgGlyArgHisArgGlyAlaProAlaArgLysArgArgGlyCys 76
QY      250 TTGGGCCCTGTATTGGTCTGCTCGGCCAAACACGAAGCTCATGAACCTTGACCTGCTTCA 191
Db      77 SerGly-----SerAlaalaArgArgArgSer-----Gly 88
QY      190 TCCTTCTGCTCTTGCGATGTCCA-----GGGACTCGAAGAAGGCGCAGCAGCTCCG 143
Db      89 AlaalaArgProProCysProArgProGlySerGlyArgArgArgGlyThrAlaPro 108
QY      142 GGTGAGCCAGCACCTTTATCGTAGAAGGTGTCAACGCCGAGCTTTCATGCTTCTGCGCGCGC 83

```

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|      | : : : | : : : | : : : |||||
Db 123 o-----ArgAArgAlaIleProTPrArgValArgArgThrProValHisAlaArgMe 141
Qy 336 -----GAGCGTGCA-----AGAGATGGCGGTCAAGC 361
Db 141 tAlaAlaGlyAlaAlaValProAlaThrGlyAspArgArgArgGlyArgAl 161
Qy 362 AGGATGTGATCCACAGCCGCCGAGTGTGGGA-----GTCCACC CGCACGAATTG 415
Db 161 aAlaAlaLeuProGluAlaHisArgSerGlyGlyArgAlaValProArg- 178
Qy 416 ACTTNCCCAACTGCGCACCCAACTGATTTTCATTAAACCCACCGCTGAGCGCT 475
Db 178 ----- 178
Qy 476 CATTCCATCGATTTTGAGCGGGAGCGCCAG-----TTGCCGAGCGC 517
Db 179 -LeuProArgValGlnGlyArgHisAlaGlyHisAlaGlyValLeuProPro 198
Qy 518 GCCCAGGGGCCCAGG 533
Db 198 oArgArgAlaProArg 203

RESULT 15
US-10-425-114-63797
; Sequence 63797, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63797
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-OSFLM202018P10_FLI.pep
US-10-425-114-63797

Alignment Scores:
Pred. No.: 0.0435 Length: 517
Score: 115.50 Matches: 62
Percent Similarity: 35.6% Conservative: 16
Best Local Similarity: 28.3% Mismatches: 80
Query Match: 10.3% Indels: 61
DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-10-425-114-63797 (1-517)
Qy 24 CAGCACACAGAGACGGCGGA-----AGCGGGATG 53
Db 89 ArgHisGlyArgAspAlaGlyGlyProArgHisProAlaAspArgThrAlaGlyArg 108
Qy 54 CGGCGCGCAAGAAGCTGTTTGATGACCTGGGCGGCAGAGCATGAAGCTGGCGTTGA 113
Db 109 HiSaLaAspArgGlyGlnHisValProGlyArgArgAlaArgGluArgArgGlyGln 128
Qy 114 CACCTT-----CTACGATAAGTGTGGCTGACCCCGAGCTGTGCCCTTCTTCCA 164
Db 129 HisCyehisAlaHisHisAggluAspAlaAlaTrpProGlyAlaArgValLeu---- 146
Qy 165 GTCCCTGCACATGCA-----AGACGA 185
Db 147 GlyProGlyHisAlaGlyValProArgArgAspValAlaAlaValaAlaArgVal 166
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QY 186 GAAGATGACGAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGG 245
Db 167 HisLeuArgLeuProAlaValHisGlnArgValProHisArgGlnProAspGln--- 185
QY 246 CCGAAGCATGTACGACGC-----ACAGGCCCATCTGGT--- 278
Db 186 LeuArgHisValAlaAlaAspProArgValGlyMetAlaProValAlaArgProArgGlyVal 205
QY 279 -----CAAGGCCACGGCCTGGACCCGCCACTTTGACAAGATCAAGCAGTA 326
Db 206 ProGlyArgArgHisGlyArgGlyValHisProGlyHisAlaGlnProGly 225
QY 327 CCTTGGAGACGCT-----GCAAGAGATGGCGCT 356
Db 226 ProAlaArgGluAlaArgProArgProArgArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY 357 CAAGCAGGATGTGATCCAGCAGCCGCCGAGTGGTGGAGTCCACCCGCCAGCAATTGA 416
Db 246 Arg-----ArgArgArgValGlnArgHisProArgArgArgGly 259
QY 417 CTNCCCAACAACCTGGCCACCCAACTGATTTTCATTAAACCAACCCCGAGCTGAGCGCTC 476
Db 260 AlaArgProGlnGluArgGlyArgValProAlaAspProAla-----AlaArg 276
QY 477 ATTCCATCGATTTTGACGGGGAGCGCCAGTTGCCGAGCGCGCCAGGGGGCCCGAGG 533
Db 277 ValProAlaValProGlyHisGlyHisArgValProGlyValProGlnProHisArg 295
```

Search completed: February 27, 2006, 09:18:53  
Job time : 157.5 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
C 1	104	9.3	1733	7	US-11-182-016-21	Sequence 2
C 2	101.5	9.0	279	7	US-11-072-512-3382	Sequence 3
C 3	99.5	8.9	1742	7	US-11-182-016-23	Sequence 2
C 4	98.5	8.8	495	7	US-11-182-016-31	Sequence 3
C 5	93.5	8.3	1730	7	US-11-182-016-19	Sequence 1
C 6	89.5	8.0	205	6	US-10-689-742-72	Sequence 7
C 7	89.5	8.0	226	7	US-11-148-012-2	Sequence 2
C 8	89.5	8.0	891	7	US-11-182-016-38	Sequence 3
C 9	88	7.8	495	7	US-11-182-016-31	Sequence 3

```
Db 656 CysProLeuLeuLeuGluProAlaGlnGlyProLeuPro-----HisSer 670
||| ||||| ||||| ||||| |||||
Qy 496 CCGCTCAAAATCGATGAAATGAGCGCTCAGCGTGGGTGGTTAATGAAATCAGTTGG 437
||| ||||| ||||| ||||| |||||
Db 671 ProLeuHisMetGly-----ProGlySerAenGlyMetGlyLeuAlaVal 685
||| ||||| ||||| ||||| |||||
Qy 436 GTGGCAGTTGTTGGGNAAGTCAAAATTCGTCGGGGTGG----- 398
||| ||||| ||||| ||||| |||||
Db 686 AlaGlnGlyCysTrpGlyAla---AlaArgSerGlyTrpAlaArgGlyCysGlyAlaPro 704
||| ||||| ||||| ||||| |||||
Qy 397 -----ACT 395
||| ||||| ||||| ||||| |||||
Db 705 ThrGlyProLeuHisCysTrpHisArgLeuProAlaValValGlySerProValGlySer 724
||| ||||| ||||| ||||| |||||
Qy 394 CCACCACTCGGGCGGTGTCGATCAT-----CCTGCTTGA 356
||| ||||| ||||| ||||| |||||
Db 725 ProProLeuProGlyValAlaGlySerSerLeuAlaLeuGlySerGlyProGlySer 744
||| ||||| ||||| ||||| |||||
Qy 355 CGCCCATCTCTTCGAGCGTCTCTCCAAGGTACTGCTTGATCTTCAAGTGGCGGTGT 296
||| ||||| ||||| ||||| |||||
Db 745 GlyProLeuLeuAlaGlyLeuLeu-----GlyCysPro-----Gly 756
||| ||||| ||||| ||||| |||||
Qy 295 CCAGCGCTGCGCTTACACAGATGGCGTGTGCGTGTATCATCTTCGCGCCCTTGATT 236
||| ||||| ||||| ||||| |||||
Db 757 ProGlyProGlyProAlaSerProGlyArgCysArgHisTrpAlaLeuGlyProAlaAla 776
||| ||||| ||||| ||||| |||||
Qy 235 GGT-----CTGCTCCGCCAACACGACGAC 212
||| ||||| ||||| ||||| |||||
Db 777 GlyProValGlnProAlaGlnProProAspProAlaGlnLeuLeuProAlaGlnSer 796
||| ||||| ||||| ||||| |||||
Qy 211 TCATGAAT-----TGACCTGCTTCATCTCTCTCTGTGCA----- 176
||| ||||| ||||| ||||| |||||
Db 797 ProHisProProIleHisValProAlaGlyArgSerAlaValAlaAlaGlyProAspGly 816
||| ||||| ||||| ||||| |||||
Qy 175 -----TGTCCAGGACTCGAAGAGGCGCAGCAGCT----- 146
||| ||||| ||||| ||||| |||||
Db 817 GlyHisSerGlnProAlaProAlaValGlnArgTrpProAlaProSerGlyArgTrp 836
||| ||||| ||||| ||||| |||||
Qy 145 -----CCGGTTCAGCCAGCACCTTATCGT 122
||| ||||| ||||| ||||| |||||
Db 837 HisSerProGluProGlyProProValProGlyProGlyAlaProGlyProGlnArg 856
||| ||||| ||||| ||||| |||||
Qy 121 AGA-----AGGTGTCA-ACGCCAGCTTC 99
||| ||||| ||||| ||||| |||||
Db 857 LysHisGlyIleAlaAlaLeuSerProAlaGlyGlnThrArgCysProGlnAlaGlnSer 876
||| ||||| ||||| ||||| |||||
Qy 98 ATGCTCTCTGCGCGCCAGGTCTCAACAGCTTCTTTCGCGCCG-----CATCCCGCTTCC 42
||| ||||| ||||| ||||| |||||
Db 877 LeuProAlaAlaProProLeuGlyProArgAlaThrAlaThrProAlaGlyValAlaAla 896
||| ||||| ||||| ||||| |||||
Qy 41 GCCGTCTCTGTGTGGTGGCGCGCTCTGCAGC 6
||| ||||| ||||| ||||| |||||
Db 897 GlyThrAlaAlaAlaLeuAlaAlaAlaArgAlaGly 908
||| ||||| ||||| ||||| |||||

RESULT 2
US-11-072-512-3382
; Sequence 3382, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
```

```
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3382
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3382

Alignment Scores:
Pred. No.: 0.0606 Length: 279
Score: 101.50 Matches: 55
Percent Similarity: 31.6% Conservative: 10
Best Local Similarity: 26.7% Mismatches: 67
Query Match: 9.0% Indels: 75
DB: 7 Gaps: 11

US-09-920-953-2 (1-598) x US-11-072-512-3382 (1-279)
Qy 528 GCCCCTCGGGCGCTCGCAAC-----TGGCGCTCCCGCTC 491
||| ||||| ||||| ||||| |||||
Db 37 SerProTrpAlaSerSerSerTrpArgAlaAlaLeuTrpSerTrpArgProProArg 56
||| ||||| ||||| ||||| |||||
Qy 490 AAAATCGATCGAATGAGCGCTCAGGCTGGGTGGTTAATGAAATCAGTTGGTGGCGC 431
||| ||||| ||||| ||||| |||||
Db 57 SerSerProSerLeuLeuArgGlyProGlyArg-----AlaPro 71
||| ||||| ||||| ||||| |||||
Qy 430 AGTTGTTGGNAGTCAAAATTCGTCGGGTGCACTCCACCACCTCCGGCGCGTGTGGA 371
||| ||||| ||||| ||||| |||||
Db 72 ThrCysTrpProLeuArgValArgMetProTrp-----ArgAlaGly 85
||| ||||| ||||| ||||| |||||
Qy 370 TCACATCTCTGTCAGCCCATCTCTTCAGCGCTCTCTCCAGGTACTGCTGATCTTGT 311
||| ||||| ||||| ||||| |||||
Db 86 SerArgProCysArgValProAlaSerThr-----ThrCys 97
||| ||||| ||||| ||||| |||||
Qy 310 CAAAGTGG-----CGGTGTCAGGCGCGTGGCCCTTG---ACCAGATGGCGGTG 263
||| ||||| ||||| ||||| |||||
Db 98 --GlyTrpTrpCysAlaSerTrpSerSerTrpArgLeuTrpValAlaTrpProCysP 117
||| ||||| ||||| ||||| |||||
Qy 262 CGTCTGATCATGCTTCGCCCTTGT----- 239
||| ||||| ||||| ||||| |||||
Db 117 roSer--ProSerProSerProCysProCysProArgProCysProLeuProTrpProGln 136
||| ||||| ||||| ||||| |||||
Qy 238 -----ATTGCTCTGCTCCGCCAAACACGAAGCTCATGAACCTTGACCTGCTCATCTTCT 185
||| ||||| ||||| ||||| |||||
Db 137 SerHisProCysLeuLeuProGlnProArgSerGln----- 148
||| ||||| ||||| ||||| |||||
Qy 184 GCTCTTGCATGTCAGGAGCTCGAAGAAGGCGCAGCTCCGGGTACGACGACCTTAT 125
||| ||||| ||||| ||||| |||||
Db 149 -----ProCysPro-----CysProAlaGlyProValProSer 159
||| ||||| ||||| ||||| |||||
Qy 124 CGTAGAAGGTGTCAACGCCAGCTTATGCTTTCGGCGCGCCAGGT----- 77
||| ||||| ||||| ||||| |||||
Db 160 ArgProArgArgMetAlaAlaLeuSerGlyAlaLeuArgProProSerGlyLeuAspPro 179
||| ||||| ||||| ||||| |||||
Qy 76 -----CATCAACAGCTTCTTGGCGCGCATCCGCTTCCCGCTCTCTCTGG 29
||| ||||| ||||| ||||| |||||
Db 180 SerProLeuHisHisArgLeuAlaAlaGlyProArgHisProThrGlyPro-----Trp 197
||| ||||| ||||| ||||| |||||
Qy 28 TGCTGTGGCGC 17
||| ||||| ||||| ||||| |||||
```

Db 198 ThrTrpProPro 201

## RESULT 3

US-11-182-016-23  
; Sequence 23, Application US/11182016  
; Publication No. US20060019294A1  
; GENERAL INFORMATION:

; APPLICANT: SUGEN, INC.  
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS  
; FILE REFERENCE: 038602/0102  
; CURRENT APPLICATION NUMBER: US/11/182,016  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US/09/958,359  
; PRIOR FILING DATE: 2002-02-05  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 1742  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Grub

US-11-182-016-23

Alignment Scores:  
Pred. No.: 0.108 Length: 1742  
Score: 99.50 Matches: 66  
Percent Similarity: 37.0% Conservative: 8  
Best Local Similarity: 33.0% Mismatches: 45  
Query Match: 8.9% Indels: 81  
DB: 7 Gaps: 15

US-09-920-953-2 (1-598) x US-11-182-016-23 (1-1742)

QY	526	CGCTGGCGCGCTCGGCACTGGCGCTCCCGCTCAAAATCGATGATGAGCGCTAG	467
Db	681	ProHisGlyAlaArgGluGlnTrp-----AspGly-----AlaGly	692
QY	466	GCTGGGGTTGGGTTAATGAAATCACTGGGTGGCGAGTTGTTGGGNAAGTCAAAATCGT	407
Db	693	ArgGlyProGlyLeuLeuGlySerSer-----LysGluLeuArg	705
QY	406	CGCGGG-----TGGACTCCACCACTC-----CGG	383
Db	706	LeuGlyGluGlyLeuArgGlyProHisTrpAlaProProLeuLeuAlaProSerAlaArg	725
QY	382	CGCGGTGCTGGATCATCTCTGCTGACGCCCA---TCTCTGACGCGTCTCTCCAGGT	326
Db	726	ArgArg-----ArgProArgGlyLeuAlaSer--SerProArgC	738
QY	325	ACTGCTTGATCTTGTCAAAGTGGCGGTGTTCAGCGCGTGGCCTTGACAGATGGCGT	266
Db	738	ysCysTrpLeuLeuSerSerSerTrpGlnArgAlaTrpGlnArg--ProHisSerArg	757
QY	265	GTGCGGTGTACATGCTTCGCGCCTTGTATTTGCTGCTCCGC-----CAACACCA	215
Db	758	-----ArgAlaAlaGlyLeuProArgSerArgAlaArgAlaArg	770
QY	214	AGCTGATGAACTGACTGCTGCTTCATCTCTGCTCTGCTGATGTCAGGAGTCCAGAGG	155
Db	771	IleSerTrpLysValProAlaLeuGlySer-----GlyAlaArgArgArg	785
QY	154	GCAGCAGCT-----CGGGTTCAGCCAGCACTTATCGTAGAGGTGT	113
Db	786	AlaSerAlaAlaSerThrAlaSerArgProGly---ProAlaProAlaSerArg-----	802
QY	112	CAACGCCCGCAGCTTCATGCTCTTCTGCGCGCCAGGTCATCAACAGCTTCTTGGCGCCG	53
Db	803	AlaLysProSerSer-----ThrHisSerCysAla---812	
QY	52	ATCCCGCTTCCGCGCTCTCTGTTGTTGCTGTGTGCGCGCTGTGAGCAGCGC	1
Db	813	-----CysTrpLysLysArg--CysSerArgArg	821

## RESULT 4

US-11-182-016-31  
; Sequence 31, Application US/11182016  
; Publication No. US20060019294A1  
; GENERAL INFORMATION:

; APPLICANT: SUGEN, INC.  
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS  
; FILE REFERENCE: 038602/0102  
; CURRENT APPLICATION NUMBER: US/11/182,016  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US/09/958,359  
; PRIOR FILING DATE: 2002-02-05  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Tks 118

US-11-182-016-31

Alignment Scores:  
Pred. No.: 0.12 Length: 495  
Score: 99.50 Matches: 64  
Percent Similarity: 31.9% Conservative: 18  
Best Local Similarity: 24.9% Mismatches: 62  
Query Match: 8.8% Indels: 113  
DB: 7 Gaps: 15

US-09-920-953-2 (1-598) x US-11-182-016-31 (1-495)

QY	531	TGGGCGCCCTGGCGCGCTCGGCAACTGGCGCTCCCGCTCAAAATCGATGATGAGCG	472
Db	179	TrpAlaPro-----AlaProGlnGlnGlyAspLeuProTrpAla	191
QY	471	CTCAGCTGGGTTGGGTTAATGAAATCAGTTGGGTGCGCAGTTGTTGGGNAAGTCAA	412
Db	192	LeuArg--TrpGlnGlnLeuAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu	210
QY	411	TTCGTGGGGTGGGAGTCCACCCTCCGCGCGGTGCTGGATCAGATCCTCTGTTGACGC	352
Db	210	rAlaGlyArgGlySerSerAlaCysGlnAlaGluAspTrp-----	223
QY	351	CATCTCTTGCAGCGTCTCTCCAAGTACTGCTGATCTTGTCAAAGTGGCGGTGTCAG	292
Db	224	-----ArgTrpArgTrp-----Tr	228
QY	291	GCCGTGGCCCTTG-----ACCAGATGGCGGTGTCGTCGTA	256
Db	228	pThrTrpProSerProSerAlaLysSerProSerGlyAlaArgGlnTrpProAlaHisph	248
QY	255	C---ATGCTTGGCGCCTTGTATGCTGCTGCTCGCCCAACACAGAGCTCA-----	205
Db	248	eclySerLeuLysProLeuLeuAlaAlaAlaProThrSerCys--SerGlyGlyTrpProA	268
QY	204	CTTGACCTGCTTCATCTCTGCTCTTGCATGTCAGGAGTCCAGGAGTCCAGAGGCGAG	148
Db	268	rgHisProAlaProAspSer-----AlaAlaProGlyValGlnProHisAlaAlaHisA	286
QY	147	CTCCGGGTGAGCAGCAGCCTTAT-----CGTAGAGGTGTCAACGCCAG	103
Db	286	laProGlyAlaProAlaProAlaAlaAlaValProArgProAlaAlaPheProProA	306
QY	102	CT-----TCATGCTTCTGCGC-----86	
Db	306	laaSpGlySerProProProSerLeuLeuTrpProArgSerCysLeuTrpGlnProPhes	326
QY	85	-----CGCC	82
Db	326	erGlnThrArgHisTrpSerSerGlyThrGlnSerProLeuGlyProGlyValProArgP	346

```
QY 81 CAGGTCAAT-----CAAACAG 67
Db 346 roGlySerGlyHisSerProCysGluSerCysSerTrpHisLeuLysProTrpProS 366
QY 66 CTTCTTGGCGCGCATCCCGTTCCGCGC-----38
Db 366 erProCysThrGlnAlaProHisProArgProValArgTrpSerHisGlyProProS 386
QY 37 --TCTCTGTGTGCTGG-----TGGCGCGCTCTGCAGGCAGCG 2
Db 386 erGlySerTrpProTrpCysArgGlyTrpHisArgLeuProSerAla 401

RESULT 5
US-11-182-016-19
; Sequence 19, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; PRIOR FILING DATE: 2005-07-15
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 1730
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Grub
US-11-182-016-19

Alignment Scores:
Pred. No.: 0.381 Length: 1730
Score: 93.50 Matches: 50
Percent Similarity: 38.9% Conservative: 32
Best Local Similarity: 23.7% Mismatches: 86
Query Match: 8.3% Indels: 43
DB: 7 Gaps: 10

US-09-920-953-2 (1-598) x US-11-182-016-19 (1-1730)
QY 583 TGGCTGATGCTCTTCAATGACGAGCGGTGGCAACAGATTTCAGGCTCTGGGCCCC 524
Db 1230 TrpArgLeuAlaLeuThrCysPro-----GluProCysSerSerLeuTrpAsnSer 1246
QY 523 CTGGGCGCGCTCGGCAACTCGCGCTCCCGCTCAAAATCGATGGAATGAGCGCTCAGGCT 464
Db 1247 LeuGlyMetGlyGlySerTrpArgSerSerGlyLysLeu---GlyLeuSerSerValLeu 1265
QY 463 GGGGTGGGTAAATGAAATCAGTTGG-----GTGCGC 431
Db 1266 SerAlaGlyProLeuGlyLeuLeuTyTrSerCysSerGlyAsnLysArgProValAlaGlu 1285
QY 430 AGTTGTTGG-----GNAAGTCAATTCGTCCGCGGTGAGCTCCACCA 389
Db 1286 ThrCysTrpProTrpArgCysValAlaValArgSerArgArgSerSerCys 1305
QY 388 CTCGGCGCGGTGCTGGATCACATCTCTTGACGCCCATCTCTTGAGCGTCTCTCCAA 329
Db 1306 IleGluThrProSerLeuSerValAlaGluArgSerAlaPheAlaMetSerPheSer 1325
QY 328 GGTACTGCTTATCTTCAAGAGGGCGGTGGTCCAGCGCGTCCCGCTTACCAGATGGG 269
Db 1326 SerSerIleSerSerCysSerAlaSerSerArgAlaLeuLysGly-----1341
QY 268 CGTGTGGCTGTACATGCTTC-----GGCCCTGTGATTGCTGTGCTCCGCCAACACGA 215
Db 1342 -----GlnArgCysLeuPheThrSerArgProLeuArgLeuIleTrpGlyGlnLys 1359
QY 214 AGCTCATGAATTTGACCTGCTTCATCTTCTGCTCTTCATGT-----CCAGGGGACT 164
```

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Db 1360 ThrSerGlyThr-----AlaaspSerAlaLeuSerCysGlyPheGlyGlyVal 1376
QY 163 CGAAGNAGG-----CCAGCAGCTCCGGTCCAGCCAGCCTTATCGTAGAAGGTGT 113
Db 1377 HisGluArgHisThrLeuCysArgGlnProHisGlnArgSerAsnSerSerGlyGlnVal 1396
QY 112 CAACCCCGCAGCTCATGCTTCTGCGCCGCCAGGTGCATCAACACAGCTTCTTCCGCCCGC 53
Db 1397 LeuLeuProSerCysGlyAspArgGlnProThrThrArgSerSerGluCysSerArg 1416
QY 52 ATCCCGCTTCCCGCGTCTCTGTGGTCTGTGGTGG 20
Db 1417 -----TrpCysProTrp 1420

RESULT 6
US-10-689-742-72
; Sequence 72, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaVallie, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-72

Alignment Scores:
Pred. No.: 0.735 Length: 205
Score: 89.50 Matches: 42
Percent Similarity: 29.6% Conservative: 19
Best Local Similarity: 20.4% Mismatches: 70
Query Match: 8.0% Indels: 75
DB: 6 Gaps: 7

US-09-920-953-2 (1-598) x US-10-689-742-72 (1-205)
QY 520 GGCGCGCTCGCAACTGGCGCTCCCGCTCAAAATCGATGGAATGAGCGCTCAGGCTGGG 461
Db 4 GlyGlyLeuGlyAlaTrpSerAlaGlySerSerValSerAlaPheHisSerThrAsnAla 23
QY 460 GTTGGGTTTAAATGAAATCAGTTGGTGGCGAGTTGTTGGGNAAGTCAAAATTCGCGCGG 401
Db 24 ValSerValPheSerLeuSerLeuPheArgAlaCysThrProValProAspProAlaPro 43
QY 400 TGGACTCCACCATCCCGCGCGCTGCTGGATCACATCTCTGTTGACGCCCATCTCTTGCA 341
Db 44 TrpProIleProCysArgGlyAlaSerGly-----53
QY 340 GCGTCTCTCCAGGTAATGCTTGTGATCTTGTCAAAGTGGCGGTGGTCCAGGCCGTGGCCCT 281
Db 54 -----LysLysThrGlyArgProAlaArg-----61
QY 280 TGACACAGATGGCGGTGGTGGT-----257
Db 62 -----AlaArgLeuArgGlyHisProAlaSerProProThrAlaArgCysLeu 78
QY 256 ACATGCTTCGGCCCTTGTATTGTTGCTGCTCCGCCAAACAGAACTCATGAATGACCT 197
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Db 79 ThrCysPhe-----AlaThrAspSerCysSerGlnPro 89  
QY 196 GTTCACTTCCTGCTCTTCATGTCAGGACTCGAAGAGGCGACGACTCGGGTCTAG 137  
Db 90 LeuGlyAlaSerValPheGlyValGlyGluLeuLeuArgAspCysAla-----Arg 106  
QY 136 CCAGCACCTTATCGTAGAGGTCTCAA-----CGCCAGCT 101  
Db 107 ProArgProProThrLeuLysCysGlnHisGlnHisGlnPheArgHisThr 126  
QY 100 TCATGCTCTTCGCGCGCGCAGGTCTATCAACAGCTTCTTGGCGCGCATC-----50  
Db 127 AlaLeuArgThrArgArgProGlyArgPheValSerSerCysIleLysLeuSerProCys 146  
QY 49 -----CCGCTTCGCGCTCT 35  
Db 147 ProLeuLeuProLeuProValPheLeuLeuPhePheSerProPheProSer 166  
QY 34 CTGTGCTGCTGTGGCGG 17  
Db 167 LeuSerAlaPhePhePro 172

## RESULT 7

US-11-148-012-2  
; Sequence 2, Application US/11148012  
; Publication No. US20060008798A1  
; GENERAL INFORMATION:  
; APPLICANT: Chien, David Ying  
; APPLICANT: Rang, Yiu-Lian  
; APPLICANT: Tabrizi, Arita  
; TITLE OF INVENTION: RABBIT MONOCLONAL ANTIBODIES TO HEPATITIS B SURFACE ANTIGENS AND  
; FILE REFERENCE: METHODS OF USING THE SAME  
; CURRENT APPLICATION NUMBER: US/11/148,012  
; PRIOR FILING DATE: 2005-06-07  
; PRIOR APPLICATION NUMBER: 60/577,561  
; PRIOR FILING DATE: 2004-06-07  
; PRIOR APPLICATION NUMBER: 60/583,734  
; PRIOR FILING DATE: 2004-06-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 226  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: amino acid sequence for the sag wild-type adw antigen  
US-11-148-012-2

Alignment Scores:  
Pred. No.: 0.741 Length: 226  
Score: 89.50 Matches: 43  
Percent Similarity: 31.2% Conservative: 17  
Best Local Similarity: 22.4% Mismatches: 54  
Query Match: 8.0% Indels: 78  
DB: 7 Gaps: 11

US-09-920-953-2 (1-598) x US-11-148-012-2 (1-226)

QY 512 CGCAACTGCGCTCCCGCTCAAAATCGATGGAATGAGGCTCAGGCTGGGGTGGGT 453  
Db 24 ArgIleLeuThrIlePro-----GlnSerLeuAspSerTrp---TrpThr 37  
QY 452 AATGAAATCAGTTGGTGGCGAG-----TTGTTGGGAAGTCAAAATCGCTCGCGGG 399  
Db 38 SerLeuAsnPheLeuGlyGlySerProValCysLeuGlyGlnAsnSerGlnSerProThr 57  
QY 398 GACTCCACCACTCCGCGCGGCTCTGGATCACATCTGCTTCAGCCCATCTCTTCAGC 339  
Db 58 SerAsnHisSerProThrSerCys-----65  
QY 338 GTCTCTCAAGGACTGCTTGATCTTTCAAGTGGCGGTGGTCCAGGCGGTGGCCCTTG 279

Db 66 -----ProProIleCys-----ProGly 71  
QY 278 ACCAGATGGCGTGGCTGGTACATGCTTCGGCCTTGTATTGGTCTGCTCGCCCAAC 219  
Db 72 TyrArgTrpMetCysLeuArgArgPheIleIlePheLeuPhe-----85  
QY 218 ACGAGACTCATGAACCTGACCTGCTTCATCTTC-----186  
Db 86 -----IleLeuLeuLeuCysLeuIleLeuLeuValLeuLeuAspTyrGlnGly 102  
QY 185 -----TGCTCTTCATGCTCCAGGACTCGAAGAGGCGAGCAGCTCCGGGTCA 138  
Db 103 MetLeuProValCysProLeuIle-ProGlyThrThrThrThrSerThrGlyPro-----120  
QY 137 GCCAGACCTTATCGTAGAGGTGTCAACCGCCAGCT-----TC 99  
Db 121 -----CysLysThrCysThrThrProAlaGlnGlyAsnSerMetPheProse 136  
QY 98 ATGCTTCTGCGCGCGCAGGTCTCAACAGCTTCTTGGCGCGCAGCTCCCGCTCCGCC 39  
Db 136 rCysCysThrLysProSerAspGlyAsnCysThrCys-----IleProIleProse 154  
QY 38 GTCT-----CTGTGGTGTGG 23  
Db 154 rSerTrpAlaPheAlaLysTyrLeuTrpGluTrp 165

## RESULT 8

US-11-182-016-38  
; Sequence 38, Application US/11182016  
; Publication No. US20060019294A1  
; GENERAL INFORMATION:  
; APPLICANT: SUGEN, INC.  
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS  
; FILE REFERENCE: 038602/0102  
; CURRENT APPLICATION NUMBER: US/11/182,016  
; CURRENT FILING DATE: 2005-07-15  
; PRIOR APPLICATION NUMBER: US/09/958,359  
; PRIOR FILING DATE: 2002-02-05  
; NUMBER OF SEQ ID NOS: 55  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 891  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Tks 202  
US-11-182-016-38

Alignment Scores:  
Pred. No.: 0.835 Length: 891  
Score: 89.50 Matches: 58  
Percent Similarity: 34.1% Conservative: 13  
Best Local Similarity: 27.9% Mismatches: 68  
Query Match: 8.0% Indels: 69  
DB: 7 Gaps: 12

US-09-920-953-2 (1-598) x US-11-182-016-38 (1-891)

QY 535 CTCCTGGGCGCCCTGGGCGGCTCGCG-----AACTGG 503  
Db 643 IleLeuAlaProGlnGlyCysPheGlyThrArgTyrLeuAlaLeuLeuTrpGluThrTrp 662  
QY 502 CGCTCCCGCTCAAAATCGATGGAATGAGGCTCAGGCTGGGGTGGGTTAATGAAATC 443  
Db 663 LeuArgProGlnValAlaProGlyAsnProAlaLysProGly-----ArgAsp 678  
QY 442 AGTTGGTGGCGAGTTGTGGGNAAGT-----416  
Db 679 SerProGlyArgThrArgTrpProAlaProProArgProArgLeuArgProPro 698  
QY 415 CAAATTCGTGGGTGGAGTCCACCACTCCCGCGGCTGGTGGATCATCATCTGCTTGA 356



Percent Similarity:	35.5%	Conservative:	16
Best Local Similarity:	26.9%	Mismatches:	53
Query Match:	7.8%	Indels:	67
DB:	7	Gaps:	10

US-09-920-953-2 (1-598) x US-11-087-227-79 (1-173)

Qy		595	TTGGTGCAGAAATGGCTGATGGCTCTTCAAATGCACGAAGGGCTGCCAACAAGATTTCGAGG	536
Db		42	MetValArgArgPheLeuValThrLeuArg-----IleArgArg	54
Qy		535	CTCCTGGCGCCCTCGGGCGCG-----CTCGGCAC	506
Db		55	AlaCysGlyProProArgValArgValPheValHisIleProArgLeuThrGlyGlu	74
Qy		505	TGGCGCTCCCCGCTCAAAAATCGATGGAATGAGCGCTCAGGCTGGGGGTTCGGGTAAATGAA	446
Db		75	TyrAlaalaPro-----GlyAlaProAlaAlaValAlaLeuVal---	87
Qy		445	ATCATGTTGGGTGCCAGATTGTTGGNAAGTCAAATTTCGTCCGGGTGGACTCCACCATC	386
Db		88	LeuMetLeuLeuArgSer-----GlnArgLeuGlyGlnGlnProLeu	101
Qy		385	CGGCGGCGTGCTGCATCACATCTCTGCTTGACGCCCATCTCTTGACGCGTCTCTCCAAGT	326
Db		102	ProArgArgProGlyHisAspaspGlycylnArgProSerGlyGlyAlaAla-----	118
Qy		325	ACTGCTTGATCTTGTCAAAGTGGCGGTGTCACAGGCGGTGCCCTTGACCAGATGGCGCT	266
Db		119	-----AlaAlaProArgArgGly-----	124
Qy		265	GTGCGTCGTACATGCTTCGGCCCTTGATTGGTCTGCTCCCGCCAAACACGAAGCTCATGA	206
Db		125	-----AlaGlnLeuArgArgProArgHisSer----	133
Qy		205	ACTTGACCTGCTTCATCTTCTGCTCTTCGATGTCAGG-----ACTCGAAGAAGG	155
Db		134	-----HisProThrArgAlaAlaArgCysProGlyGlyLeuProGlyHisAlaGly	150
Qy		154	GCAGCAGCTCGGGTCAGCCAGCACCTTATCGTAGAGGTGTCAACCCGCCAGCTTCATCG	95
Db		151	GlyAlaalaProGlyArgglyAlaalaGlyArgalaArgCysLeuGlyProSerAla----	169

DD FORM 1-70 (Rev. 1-67) 1-70

RESULT 12

RESULT 12  
HS-11-196-721-5

US-II-186-731-3  
: Sequence 5. Application US/11186731

Sequence 3; Application 00/1100751  
; Publication No. US2005025521A1

; GENERAL INFORMATION:

APPLICANT: Kapeller-Libermann, Rosana

APPLICANT: Acton, Susan L.

;  
: TITLE OF INVENTION: 39079 and 12399, PROCEIN KINASE FAMILY  
: TITLE OF INVENTION: Members and Uses Therefor

```

; FILE OF INVENTION: INVENTED AND USED IN INVENTION
; FILE REFERENCE: MPI2001-047P1RCP1 (M)

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;; CURRENT APPLICATION NUMBER: US/11/186,731.

```
; CURRENT FILING DATE: 2005-07-21
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; PRIOR APPLICATION NUMBER: US/10/077,130  
 ; PRIOR FILING DATE: 2002-03-15

; PRIOR FILING DATE: 2002-02-13  
 ; PRIOR APPLICATION NUMBER: 60/269201

; PRIOR FILING DATE: 2001-02-15

; NUMBER OF SEQ ID NOS: 9

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; SOFTWARE: FastSEQ for Windows Version 4.0
;
; CEC ID NO 35

```

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; SEQ ID NO 3
;   LENGTH: 7968

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;
; TYPE: PRT
```

ORGANISM: Homo sapiens

US-11-186-731-5

ALIMENTUM; FOOD.

Alignment scores:	
Pred. No.:	1.54
Length:	7968

Score: 87.50 Matches: 59  
Percent Similarity: 36.0% Conservative: 26  
Best Local Similarity: 25.0% Mismatches: 76  
Query Match: 7.8% Indels: 75  
DB: 7 Gaps: 13

US-09-920-953-2 (1-598) x US-11-186-731-5 (1-7968)

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QY 595 TTGTCGCGAAATGGCTGATGGCTCTTCAATGCAGCAAGGGTGGCAACGATTTCAGG 536
Db 64 LeutyArgLeuThrIleLeuAspLeuAlaLeuGlyAspSerGlyGlnTyrValCysArg 83
QY 535 CTCCTGGCGCCCTGGGC-----GCCTCGGCAACTGGCGCTCCCGCTCAAA 488
Db 84 AlaArgAsnAlaIleGlyGluAlaPheAlaValGly-----LeuGln 98
QY 487 ATCGATGGAATAGCGCT-----CAGCTGGGGTGGGTANTGAATAATCAGTTGG 437
Db 99 ValAspAlaGluAlaAlaCysAlaGluGlnAlaProHisPheLeuLeuArgProThrSer 118
QY 436 GTGCGCAGTTGTTGGNAACTCAATTCGTGCGGGTGGACTCCACCCTCGCGCGCGT 377
Db 119 IleArg-----ValArgGluGlySerGluAlaThrPheArgCysArg 132
QY 376 GCTGGATCACATCTGCTGACGCCCATCTCTTGCAGCGTCTCTCCAAGGTACTGCTTGA 317
Db 133 ValGlyGlySerPro-----ArgProAlaValSerTrpSerLysAspGlyArg----- 148
QY 316 TCTTGTCAAAAGTGGCGGTGTCAGCGCGGTGGCCCTTGACCATGGG---CCTGTGCGT 260
Db 149 -----ArgLeuGlyGluProAspGlyProArgValArg 159
QY 259 CGTACATGCTTCGGC-----CCTGTATTGTT 233
Db 160 ValGluGluLeuGlyGluAlaSerAlaLeuArgIleArgAlaAlaArgProArgAspGly 179
QY 232 CTGCTCGCCCAACACAGAACTCATGAACCTTGACCTGCTTCATCTCTCTGCTTGTGATGT 173
Db 180 GlyThrTyrgluValArgAlaGluAsnProLeuGlyAlaAlaSerAlaAlaAlaLeu 199
QY 172 -----CCAGGGACT----- 164
Db 200 ValValAspSerAspAlaAlaAspThrAlaSerArgProGlyThrSerThrAlaAlaLeu 219
QY 163 -----CGAAGAGGGCAGCAGCTCCGGGTGAGCCAGCAGCCTTATCGTAGA 119
Db 220 LeuAlaHisLeuGlnArgArgGluAlaMetArgAlaGluGlyAlaPro----- 236
QY 118 AGGTGTCAACGCCAGCT-----TCATGCTTCTGCGCGCCCGCCAGGTGTCATCA 71
Db 237 ---AlaSerProProSerThrGlyThrArgThrCysThrValThrGluGlyLysHisAla 255
QY 70 ACAGCTTCTTGC-----GCCCGATCCCGCTTCGCGCGTCTCTGTGG 29
Db 256 ArgLeuSerCysTyrgluValThrGlyGluProLysProGluThrValTrp 271
```

RESULT 13

US-11-072-512-3151  
; Sequence 3151, Application US/11072512  
; Publication No. US20060029945A1  
; GENERAL INFORMATION:  
; APPLICANT: ISOGAI, TAKAO  
; APPLICANT: SUGIYAMA, TOMOYASU  
; APPLICANT: OTSUKI, TETSUJI  
; APPLICANT: WAKAMATSU, AI  
; APPLICANT: SATO, HIROYUKI  
; APPLICANT: ISHII, SHIZUKO  
; APPLICANT: YAMAMOTO, JUN-ICHI  
; APPLICANT: ISONO, YUUKO  
; APPLICANT: HIO, YURI  
; APPLICANT: OTSUKA, KAORU  
; APPLICANT: NAGAI, KEIICHI  
; APPLICANT: IRIE, RYOTARO

```
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3151
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-072-512-3151

Alignment Scores: 1.45 Length: 354
Pred. No.: 86.50 Matches: 55
Score: 36.2% Conservative: 22
Percent Similarity: 25.8% Mismatches: 65
Best Local Similarity: 7.7% Indels: 71
Query Match: 7 Gaps: 12
DB: 12

US-09-920-953-2 (1-598) x US-11-072-512-3151 (1-354)
QY 20 CCACGACGACCA-----CAGAGACGCGGAGCGGATCGGGC----- 58
Db 137 ProProAlaProAlaProHisTrpAlaSerArgAlaArgSerAlaGlyArgThrArg 156
QY 59 -----GCAAGAAAGCTGTTTGTATGACCTGGCGGCG 88
Db 157 ArgAlaSerProProGlyAlaAlaLeuAlaSerGlySerSerArgArgGluGlyArgCys 176
QY 89 CAGAAGCATGAGTGGCGGTGTGACCTTCTACGATAAGTGC---TGG---CTGACC 142
Db 177 ArgGlnAlaArgSerProArgSerSerSerThrIleSerArgCysThrTrpGluArgThr 196
QY 143 CGGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGACAGAGAAGATGAACAGTCA 202
Db 197 ArgSerThrProProGlyPheThrAlaTrpLysThrSerSerAlaArgSerAlaValSer 216
QY 203 AGTTCATGAGCTTCGTGTTTGGCGGAGCAGACCAATACAAGGCCGGAAGCATGTACGACG 262
Db 217 ThrProAlaAlaAlaCys-----GluCysSerArg 226
QY 263 CACAGCCCATCTGTTCAAGGGCCAGCGGTGAGCACCACCGCCACTTTGACAGATCAAGC 322
Db 227 SerSerPro-----ThrSerTrpThr----- 234
QY 323 AGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGAGGATGTATCCAGCAGCGCG 382
Db 235 -----ArgSerSerArgLeuProPheProAlaProGlyLeuArgSer 244
QY 383 CCGGAGTGGTGGAGTCCACCGCGAGAAATTTGACTTNCCTCA----- 424
Db 245 SerAla-----SerProAlaProArgSerLeuProPheProAlaProGlyLeuArgSer 262
QY 425 -----ACAACTCGGCACCCAACTGATTTTCAATTAACCCAAACCCAGCCTGAGCGCT 475
Db 263 GlnArgPheSerThrSerAlaProProArgHisAlaArgProProValAlaAlaGlyAla 282
QY 476 CATTCCATCGATTTTGAGCGGGAGCGCCAGTTGCGGAGCGGCCCGCCAGGGG-----GCC 529
Db 283 -----ArgAlaAlaProProHisProGlnAlaSerGlyArgLysSer 296
QY 530 CAGGAG---CCTGCAAAATCGTTTGGCCAGCCCTTGTCTGCA 565
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	232	20.7	126	2	US-09-502-540-13031		Sequence 13031, A
C	136	12.1	345	2	US-09-252-991A-32377		Sequence 32377, A
C	134.5	12.0	170	2	US-09-252-991A-19980		Sequence 19980, A
C	134	11.9	663	2	US-09-252-991A-30843		Sequence 30843, A
C	130.5	11.6	308	2	US-09-252-991A-27249		Sequence 27249, A
C	129	11.5	1476	2	US-09-252-991A-29427		Sequence 29427, A
C	126	11.2	235	2	US-09-252-991A-24046		Sequence 24046, A
C	125.5	11.2	394	2	US-09-252-991A-19344		Sequence 19344, A
8	125.5	11.2	394	2	US-09-252-991A-19344		Sequence 19344, A
9	124	11.1	312	2	US-09-252-991A-19787		Sequence 19787, A
10	122	10.9	726	2	US-09-252-991A-20675		Sequence 20675, A
11	121.5	10.8	204	2	US-09-252-991A-17837		Sequence 17837, A
12	121.5	10.8	351	2	US-09-252-991A-18476		Sequence 18476, A

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Qy 97 ATGAAGTCGGCGTTGACACCTTCTACGATAAGTGTGCTGGTGCACCGAGCTGCTGCC 156
Db 19 MetAlaAlaValGluValPheTyrArgLysValLeuAlaAspHisSerHis 38
Qy 157 TTCTTCAGTCCCTGGACATGCAAGACAGAGATGAAGCAGGTCAAGTTCATGAGCTTC 216
Db 39 PheGluAspValAspMetGluArgGlnAlaAlaLysGlnLysAlaPheLeuThrMet 58
Qy 217 GTGTTTCGCGGAGCAGACCAATACAAGCGCGAGCATGTACGACGACACGCCCATCTG 276
Db 59 ValThrGlyGlyProValHisTyrSerGlyLysAspMetArgAlaGlyHisAlaProLeu 78
Qy 277 GTCAAGGCCACCGCTCGACCCACCGCCTTTGACAGATCAAGCAGTACCTTTGGAGAG 336
Db 79 ValLys---ArgGlyLeuAsnAspSerHisPheAspAlaValAlaGlyHisLeuLysAla 97
Qy 337 ACGTCAAGAGATGGCGGTCAAGCAGATGTGATCCAGCAGCGCCGCGGAGTGGTGAG 396
Db 98 ThrLeuGluGluLeuGlyValAlaAlaProLeuValAlaArgValMetThrIleAlaGlu 117
Qy 397 TCCACCCGC 405
Db 118 SerAlaArg 120

RESULT 2
; US-09-252-991A-32377
; Sequence 32377, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32377
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32377

Alignment Scores:
Pred. No.: 8.49e-06 Length: 345
Score: 136.00 Matches: 70
Percent Similarity: 34.8% Conservative: 10
Best Local Similarity: 30.4% Mismatches: 64
Query Match: 12.1% Indels: 86
DB: 2 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-32377 (1-345)
Qy 539 CAGCTCTGGCGCCCTGGCGCGCTCGCAACTGGCGTCCCTCC---GCTCAAAATCGA 483
Db 101 GlnGlyProGlyGlyProGlyArgAspArgGlnValArgLeuProAlaAlaProGlyArg 120
Qy 482 TGAATGAGCGCTCAGGCTGGGGTTGGTTAATGAAATCAGTTGGTGGCGCAGTTCTTG 423
Db 121 ProSerArgGln-----SerArgLeu 128
Qy 422 GGNAAGTCAATTCGTCCGGGTGGAGTCCACCACTCCGGCGGTGCTGGA----- 371
Db 129 GlnArgHisGlyLeuSerArgCysProLeu-ProLeuArgArgProSerProAla 148
Qy 370 -----TCACATCC 363
Db 148 aTrpArgGlnProProIleGluLeuGlyAlaValArgLeuArgProProGlnArgArg 168
Qy 362 TGCTTGACGCCCATCTCTTGACGGCTCTCTCCAGGCTACTGCTTGATCTTGTCAAAGTGG 303

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Db 168 oAlaGlnArgProAlaValAlaAla 176
Qy 302 CGTGGT-----CCAGGCGTGGCTTGCACAGATGGCGGTGTGCGTGTACATG 252
Db 177 -GlyGlyGlnArgGlnProGlyArgAspProAlaGluHisLeuArgProArgArgPro-- 195
Qy 251 CTTCCGCGCTTGTATTGGTCTGCTCCGCCAAACACCAAGCTCATGAACCTTGACTGCTTC 192
Db 196 -----GlyLeuLeuArgArgProArgArg-----ProAlaGln 206
Qy 191 ATCTTCTGCTTTCATGT-----CCAGGGACTCCAAGAAG 156
Db 206 nProGlyArgLeuAlaSerGlyArgGlyAlaGlyGlyAlaGluProGlySerArgArgAr 226
Qy 155 G-----CGACGAGC 147
Db 226 gGlnValProGlyArgArgArgProPheArgSerProAlaGlyAlaAspArgAlaVala 246
Qy 146 TCCGGGTGAGCCAGCACCTTATCGTAGAGGTGTCAACGCCAGCTTCATGCTCTTCGCG 87
Db 246 lProGlyGluProArgProGlyProArgArgArgArgProGluGlnArgProArgArgHi 266
Qy 86 CGCCCGAGGTCTAT---CAAACAGCTTCTTGCGCCCGCATCCCGCTTCCCGCTCTCTGTG 30
Db 266 sArgProAlaHisGlyProGlyAlaGly-TyrProAlaAlaProLeuArgArgAlaGlyG 286
Qy 29 GTGCTGGTGGCGCGCTGTCAGGCGAG 4
Db 286 lAlaThrArgHisArgLeuArgGln 294

RESULT 3
; US-09-252-991A-19980
; Sequence 19980, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19980
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19980

Alignment Scores:
Pred. No.: 9.39e-06 Length: 170
Score: 134.50 Matches: 68
Percent Similarity: 38.3% Conservative: 9
Best Local Similarity: 33.8% Mismatches: 45
Query Match: 12.0% Indels: 79
DB: 2 Gaps: 15

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)
Qy 524 CTGGGGCGCTCGGCAACTGGCGCTCCCGCTCAA-----ATCGATGAATGAGCGC 471
Db 14 ProGlyArgArgAsnArgArgAlaAlaProAlaAlaAlaGlyArgArgSerAlaArg 33
Qy 470 TCAGGCTGG-----GTTGGGTTAATGAAATCAGTTGGTGGCGAGTTGTTGGGNAAG 417
Db 34 SerGlyTrpProCysGlyTrp-----Arg-TrpSerHisProCysTrp----- 47
Qy 416 TCAAAATTCGTCCGGGTGGAGTCCACCACTCCCGCGCGTGTGGATCCATCTGCTTG 357

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US-09-252-991A-19787

Alignment Scores:  
Pred. No.: 0.000155 Length: 312  
Score: 124.00 Matches: 59  
Percent Similarity: 37.7% Conservative: 13  
Best Local Similarity: 30.9% Mismatches: 73  
Query Match: 11.1% Indels: 46  
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19787 (1-312)

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QY 9 TGCAGACGCGCCACACAGACAGACGCGGAGCGGATGCGGCGCAAGAGCT 68
DB 39 CysArgArgProGluGlnHisAlaProHisArgGlyAspGlyArgAlaTrpArg--- 57
QY 69 GTTGTAGACTGGCGCGCGCAGAGGATGAGCTGGCGGTTCACACTTCTACGATA 128
DB 58 -----GlyHisArgProSer----- 63
QY 129 GGTGCTGGTGACCCGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAA 188
DB 64 GlyLeuProArgProGlyArg-----LeuArgAlaSerAlaHisArgArgAlaGly 80
QY 189 GATGAACGAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGC-----AGACCAATA 239
DB 81 HisArgAlaGlyGlnArgHisAlaLeuProAlaTrpArgThrAlaArgIleArgProAla 100
QY 240 CAAGGCGGAGCATGTACAGCGCACAGGCCA-----TCT 275
DB 101 AlaGlyProValAlaAlaThrArgGlnAlaProArgArgAlaLeuHisAlaProGlyAla 120
QY 276 GGTCAAGCGGCACCGCTGGACCCCGCTTGGACAGATCAAGCAGTACCTTTGGAGA 335
DB 121 GlyArgGlyArgArg-----AlaProValArgArgAspProAlaThrProGlyThr 137
QY 336 GACGCT-----GCAAGAGATGGCGTCAAGCAGGATGTGATCCAGCAGCG 380
DB 138 GlyThrAlaAlaLeuLeuHisAlaArgPheGlyHisLeuAla-----HisArg 153
QY 381 CGCGGAGTGTGAGTCCACCGCGAGCAATTTGACTTCCCACTGCGCGCACCA 440
DB 154 ProGlyThrGlyProAlaAlaGlyAlaArgValLeuArgArgProArgLeuArgProGln 173
QY 441 CTGATTTTC---ATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGAGCGGG 497
DB 174 ArgLeuHisArgLeuHisProAla-----GlyArgArgProArgSerAlaAlaGly 190
QY 498 GAGCGCCAGTTGCGAGC---GCGCCCGAGGGG 527
DB 191 ArgArgGlnGlyProAlaArgLeuProArgGly 201
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RESULT 10

US-09-252-991A-20675  
; Sequence 20675, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20675  
; LENGTH: 726  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20675

Alignment Scores:

Pred. No.: 0.000349 Length: 726  
Score: 122.00 Matches: 74  
Percent Similarity: 32.1% Conservative: 6  
Best Local Similarity: 29.7% Mismatches: 74  
Query Match: 10.9% Indels: 95  
DB: 2 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)

```
QY 2 CGCTGCTGCAGACG-----CGGCCACACACACACAGCGGCGGAGCGGATGCG 55
DB 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAlaAr 318
QY 56 GCGCGCAAGAAGCTGTTTGATGACTGGCGCGCGCAGAAGG-----CATGAAGC 103
DB 318 g-----ProAlaAlaArgArgAlaAlaAlaValGlyGluAl 331
QY 104 TGSC-----GGTTGACACCTTCTACGATAAGTGTGGC-----TGACCCGAGC 148
DB 331 aGlyAlaAlaGlyGlnGlyProArgArgThrGlyAlaAlaAlaArgThrGlnSerProGlySe 351
QY 149 TGCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTCA 208
DB 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGluGlySerAla-----AlaG1 369
QY 209 TGAGCTTTCGTGTT-----TGG----- 224
DB 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
QY 225 -----CGGAGCAGACCAATACAAAG 244
DB 389 oAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
QY 245 GCGAAGCATGTACGAGGACACCGCCCACTGTCAGGCGCCAGCGCTGACCCGCC 304
DB 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProProPr 429
QY 305 ACTTTGACAA-----GATCAA-----GCAGTACCTTGGAGAGACGCTGCAAG 346
DB 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaAlaProGlyArgAspAlaAlaAr 449
QY 347 AGAT----- 350
DB 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
QY 351 -----GGCGTCAACGAGATGTGATCCAGCAGCGCGCGGAGTGTGAGT 397
DB 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyGlyAl 489
QY 398 CCACCCGCGACGAATTTGACTTCCCAACCACTGCGCACCACTGATTTTTCATTAACCC 457
DB 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
QY 458 AACCCCGAGCTGAGCGCTCATTCATCGATTTTGGCGGGAGCGCGCAGTTGCCGAGCGC 517
DB 503 o-----HisGlyArgArgHisLeuProAl 512
QY 518 GCCCGGGGGCCAGGAGCGCTGCAA 542
DB 512 aGlnArgGlyGluProAlaLeuArg 520
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RESULT 11

US-09-252-991A-17837  
; Sequence 17837, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A



APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20161  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20161

Alignment Scores:  
Pred. No.: 0.000297 Length: 248  
Score: 121.00 Matches: 47  
Percent Similarity: 35.1% Conservative: 19  
Best Local Similarity: 25.0% Mismatches: 62  
Query Match: 10.8% Indels: 60  
DB: 2 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)

QY 2 CGTGCCTGCAGACGGCGCCACAGCA---CCACAGAGACGGCGGAGAGCGGATGCGGGC 58  
| | | | | : : : : : | | | | : : : : :  
Db 56 ArgCysAlaArgSerProProAlaGlyProSerSerThrThrArgProAlaSer 75  
| | | | | : : : : : | | | | : : : : :  
QY 59 GCAAGA---AGCTGTTTGATGACCTGGCGCGCAGAGCATGACGTCGCGGTGACA 115  
| | | | | : : : : : | | | | : : : : :  
Db 76 AlaSerIleArgCys-----SerAlaArgValArgIleTrpSerThr 90  
| | | | | : : : : : | | | | : : : : :  
QY 116 CCTTCTACGATAAGG----- 130  
| | | | | : : : : : | | | | : : : : :  
Db 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgArgTrpCysArg 110  
| | | | | : : : : : | | | | : : : : :  
QY 131 -----TGCTGGCTGACCCGGAGC-----TGCTGC----- 154  
| | | | | : : : : : | | | | : : : : :  
Db 111 ArgCysAlaCysTrp---ThrArgAsnArgProAlaArgSerCysArgCysCysValAla 129  
| | | | | : : : : : | | | | : : : : :  
QY 155 -----CCTTCTTCGAGTCCCTGGACATGC 178  
| | | | | : : : : : | | | | : : : : :  
Db 130 ThrArgSerSerAlaProProThrThrProProAlaProThrSerIleProThrProCys 149  
| | | | | : : : : : | | | | : : : : :  
QY 179 AAGACGAGAAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTTGTCGGGAGCAGACCAAT 238  
| | | | | : : : : : | | | | : : : : :  
Db 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla--- 159  
| | | | | : : : : : | | | | : : : : :  
QY 239 ACAAGGCCGAAGCATCTACAGCACACGCCCATCTGGTCAAGGGCCACGGCTGGACC 298  
| | | | | : : : : : | | | | : : : : :  
Db 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTrpArgSerAlaGlySerThrAla 178  
| | | | | : : : : : | | | | : : : : :  
QY 299 ACCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGAGCTGTCAGAGATGGCGCTCA 358  
| | | | | : : : : : | | | | : : : : :  
Db 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgArgCys-----TrpSerThr 196  
| | | | | : : : : : | | | | : : : : :  
QY 359 AGCAGGATGTGATCCACAGCGCCCGAGTGGTGGAGTCCACCCGCGAGCAATTTGACT 418  
| | | | | : : : : : | | | | : : : : :  
Db 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216  
| | | | | : : : : : | | | | : : : : :  
QY 419 TNCACAACTGCGCACCCCACT 442  
| | | | | : : : : : | | | | : : : : :  
Db 217 SerProSerAlaAlaGlnProSer 224  
| | | | | : : : : : | | | | : : : : :  
RESULT 14

US-09-252-991A-20509  
; Sequence 20509, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20509  
; LENGTH: 686  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20509

Alignment Scores:  
Pred. No.: 0.000436 Length: 686  
Score: 121.00 Matches: 51  
Percent Similarity: 35.2% Conservative: 5  
Best Local Similarity: 32.1% Mismatches: 47  
Query Match: 10.8% Indels: 56  
DB: 2 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)

QY 3 GCTGCCTGCAGACGGCGCCACAGCACCACAGAGAGCGGAGCGGATGCGGGCGCAA 62  
| | | | | : : : : : | | | | : : : : :  
Db 117 AlaAlaCysArgGlyAlaTrpHis-----GlyLeuArgProArg 130  
| | | | | : : : : : | | | | : : : : :  
QY 63 GAAGCTGTTTGATGACCTGGCGCGCAGAGGAGCATGAAGTCGCGGTTGACACCTTCTA 122  
| | | | | : : : : : | | | | : : : : :  
Db 131 ProAla-----GlyArgAlaArgArgProAlaAlaGlyGly----- 142  
| | | | | : : : : : | | | | : : : : :  
QY 123 CGATAAGTGTGCTGCTGACCCCGAGAGCTGTCGCCCTTCTTCGAGTCCCTCGACATGCAAGA 182  
| | | | | : : : : : | | | | : : : : :  
Db 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155  
| | | | | : : : : : | | | | : : : : :  
QY 183 GCAGAGATGAACAGGTCAAGTTCATGAGCTTCGTTGTTGG----- 224  
| | | | | : : : : : | | | | : : : : :  
Db 156 ProAlaProArgThr-----ValAlaArgArgProTrpArgHisProArgCysAla 173  
| | | | | : : : : : | | | | : : : : :  
QY 225 -----CGGAGCAGACCAATACAAAGGCGGAGCATGTACGACGACACGCCCATCTGGT 278  
| | | | | : : : : : | | | | : : : : :  
Db 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgArgGlyAlaGly 191  
| | | | | : : : : : | | | | : : : : :  
QY 279 CAAGGCCACGGCTGGACACCGCCATTTGACAAGATCAAGCAGTACCTTGGAGAGAC 338  
| | | | | : : : : : | | | | : : : : :  
Db 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205  
| | | | | : : : : : | | | | : : : : :  
QY 339 GCTGCAAGA-----GATGGCGCTCAA 359  
| | | | | : : : : : | | | | : : : : :  
Db 206 AlaAlaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225  
| | | | | : : : : : | | | | : : : : :  
QY 360 GCAGGATGTGATCCAGCAGCCCGCGAGTGGTGA-----GTCACCCCG 404  
| | | | | : : : : : | | | | : : : : :  
Db 226 ProGlyAlaGlyAlaGlyProArgArgGlyGlyGlyValArgArgThrHisPro 244  
| | | | | : : : : : | | | | : : : : :  
RESULT 15

US-09-252-991A-23215  
; Sequence 23215, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23215  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23215

Alignment Scores:  
Pred. No.: 0.000362 Length: 219  
Score: 120.00 Matches: 57  
Percent Similarity: 38.3% Conservative: 18  
Best Local Similarity: 29.1% Mismatches: 72  
Query Match: 10.7% Indels: 49  
DB: 2 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-23215 (1-219)

```
QY 593 GGTGCGAAATGGCTGATGGCTTCAATGCGAGGCTGGCAAGGCTTGCAGGCT 534
   ||| : : : ||| ||| : : : |||
Db 58 GlyArgTyrSerAspArgSerAlaPro-----AlaAsnProProGly 73

QY 533 CTGGGCCCCCTGGGGCGGCAACTGGGGCTCCCT-----GCTCAAAATCGA 483
   ||| : : : ||| : : : ||| : : : |||
Db 74 ProGlySerValProArgSerArgTyrAlaValProGlyAlaAlaArgSerArg 93

QY 482 TCGAATGACGCTCAG-----GCTGGGTTGGTTAATGAAATCAGTTGGT 435
   : : : ||| : : : ||| : : : |||
Db 94 -ProAlaThrGlyProProArgTrpAlaGlyProGlyHisArgAlaAlaAlaTrpLe 113

QY 434 GCGCAGTTTGGGNAAGTCAAAATTCGTGCGGGTGGACTCCACACTCGGGGGGTGC 375
   : ||| : ||| : ||| : ||| : |||
Db 113 uArg-----ArgArgAlaSe 118

QY 374 TGGATCACATCTGCTTGAGCCCATCTCTTCAGCGTCTCTCCAAGGTACTGCTGATC 315
   : ||| : ||| : ||| : ||| : |||
Db 118 rAlaSerCysProGlyHisArgGlyAspSerGlySerSerProGlyProArgLysAl 138

QY 314 TTGTCAAAGTGGCGGT-----GGTCCAGCGCTGGCCCTTGACACAGATGGCGGT 264
   : : : ||| : : : ||| : : : |||
Db 138 aThrArgGlyHisGlyArgLysArgProProGlyArg-----ProAspAlaProVa 155

QY 263 GCGTCGTACATGCTTCGGCCCTTGTATTTGGTCTGCTCCGCCAAACACGAAGCTCATGAAC 204
   ||| : ||| : ||| : ||| : |||
Db 155 lArgArg-----AlaProAlaAsnSerVal----- 163

QY 203 TTGACCTGCTTCACTTCTTCTGCTTTCATGTCAGGACTCGAAGAGGCGCAGCTCC 144
   ||| : ||| : ||| : ||| : |||
Db 164 ----ProAlaSerArgGlyArgAlaGlyCysSerArgPheArgCysArgThrProAlaPr 182

QY 143 GGTCCAGCCAGCACCTTATCGTAGAAGTGTCAACCGCCAGCTTCATGCTTCTGCGCG 84
   ||| : ||| : ||| : ||| : |||
Db 182 oGlyAlaProAlaArgProAlaGlyArgSerProProAlaArgCys-----Ar 199

QY 83 CCCAGGTCAACACAGCTTCTTGGCCCGCATCCCGTTCCGCG 38
   ||| : ||| : ||| : ||| : |||
Db 199 gSerGlyCysAlaAlaAlaArgGlyProProValProValProPro 214
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Search completed: February 27, 2006, 09:14:41  
Job time : 39 secs

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